



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 123264**

**TO: Michael Borin**  
**Location: REM-2A55&2C70**  
**Art Unit: 1631**  
**June 2, 2004**

**Case Serial Number: 09/854906**

**From: P. Sheppard**  
**Location: Remsen Building**  
**Phone: (571) 272-2529**

**sheppard@uspto.gov**

### **Search Notes**

STIC-Biotech/ChemLib

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From: Borin, Michael  
Sent: Friday, May 28, 2004 4:39 PM  
To: STIC-Biotech/ChemLib  
Subject: Search request: 09/854906

123264

Examiner: M.Borin  
AU: 1631  
Mailbox:2C70  
Office: Remsen 2A55  
Tel.: 20713

CRFE

RE: 09/854906; TNFR-1

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Please conduct search of polypeptide SEQ ID 1,8,9 against the commercial protein database.

Thank you

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:30:06 ; Search time 48.9581 Seconds

(without alignments)  
646.376 Million cell updates/sec

Title: US-09-854-906-1

Perfect score: 587

Sequence: 1 MAHKPQSLDTPDPTLYAVV.....DIEALCPAALPPAPSLLR 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

1: Geneseq1980s.\*

2: Geneseq1990s.\*

3: Geneseq2000s.\*

4: Geneseq2001s.\*

5: Geneseq2002s.\*

6: Geneseq2003as.\*

7: Geneseq2003bs.\*

8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	587	100.0	112	5	Abb81751 Tumour ne
2	579	98.6	111	5	Abb81749 Tumour ne
3	579	98.6	158	5	Abg70127 Human pre
4	579	98.6	426	7	Abw00828 Human p55
5	579	98.6	453	4	Aab50895 Human TNF
6	579	98.6	455	2	Abg74755 Human TNF
7	579	98.6	455	2	Aar07451 Human Tum
8	579	98.6	455	2	Abg74751 Human TNF
9	579	98.6	455	2	Aar12550 Type I TN
10	579	98.6	455	2	Aar10986 30KD TNF
11	579	98.6	455	2	Aar11082 Human 55k
12	579	98.6	455	2	Aar20787 TNF-alpha
13	579	98.6	455	2	Aar42059 Lambda de
14	579	98.6	455	2	Aar51034 Mutant p5
15	579	98.6	455	2	Aar42197 p55 Tumou
16	579	98.6	455	2	Aar75084 p55 TNF-R
17	579	98.6	455	2	Aay30934 Human tum
18	579	98.6	455	3	Ab01336 TNF-R1 de
19	579	98.6	455	3	Ab26984 Human TNF
20	579	98.6	455	3	Ab36266 Human tum
21	579	98.6	455	3	Ab23446 Human tum
22	579	98.6	455	3	Ab37800 Human tum
23	579	98.6	455	4	Ab86817 Human TNF
24	579	98.6	455	4	Ab37677 Human 30
25	579	98.6	455	4	Ab36697 Human tum

26	579	98.6	455	5	AAU75064 Human tum
27	579	98.6	455	5	AAO22286 TNFR1 exp
28	579	98.6	455	5	ABB81649 Human tum
29	579	98.6	455	5	ABP54799 Human COP
30	579	98.6	455	6	ABP70914 Human CON
31	579	98.6	455	6	ABP58639 Human tum
32	579	98.6	455	6	ADA20581 Precursor
33	579	98.6	455	7	ADP57929 Human Pro
34	579	98.6	909	2	AAW64485 Human Fas
35	554	94.4	455	2	AAR24000 TNF-alpha
36	518	88.2	443	2	AAR51033 Mutant p5
37	466	79.4	433	2	AAR51032 Mutant p5
38	443	75.5	86	4	AAV97655 Human TNF
39	443	75.5	108	2	AAW73570 Cytoplaem
40	421	71.7	471	5	ABB98169 Bovine tu
41	421	71.7	471	5	AAE25816 Bovine tu
42	404	68.8	78	5	ABG31493 Human Apo
43	404	68.8	78	5	ADA49709 Death dom
44	394.5	67.2	84	2	AAW62179 Tumour ne
45	384	65.4	461	2	ABG74754 Rat TNF-R

#### ALIGNMENTS

##### RESULT 1

ABB81751  
ID ABB81751 standard; protein; 112 AA.

XX  
AC ABB81751;

XX  
DT 10-SEP-2002 (first entry)

XX  
DE Tumour necrosis factor receptor 1 death domain (longer sequence).

XX  
KW Tumour necrosis factor receptor 1; receptor; TNFR-1; death domain;

KW receptor signalling; TNFR-1 DD; protein co-ordinate data.

XX  
OS Unidentified.

XX  
PN US2002045578-A1.

XX  
PD 18-APR-2002.

XX  
PF 14-MAY-2001; 2001US-00854906.

XX  
PR 22-MAY-2000; 2000US-0206215P.

XX  
(SUKITS) SUKITS S F

PA (XUGG/) XU G.

PA (LINL/) LIN L.

PA (TELL/) TELLIEZ J.

PA (HSUS/) HSU S.

XX  
PI Sukits SF, Xu G, Lin L, Telliez J, Hsu S;

XX  
WPI; 2002-443412/47.

XX  
Solution comprising tumor necrosis factor receptor 1 death domain, useful

for identifying potential inhibitor of tumor necrosis factor receptor 1 death domain.

XX  
Claim 1; Fig 7; 49pp; English.

XX  
The sequence represents the tumour necrosis factor receptor 1 death domain (TNFR-1 DD), which is the intracellular functional domain responsible for the receptor signalling activities. The invention relates to a novel solution comprising a tumour necrosis factor receptor 1 death domain. The solution is useful for identifying a potential inhibitor of TNFR-1 DD, for the design and selection of potent and selective inhibitors of TNF signalling pathways, and for generating a three-dimensional structure for an unknown molecule or molecular complex

SQ Sequence 112 AA;

Query Match  
Best Local Similarity 100.0%; Score 587; DB 5; Length 112;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAHKQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSM 60  
DB 1 MAHKQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSM 60  
QY 61 LATWRRTPREATLELGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 112  
DB 61 LATWRRTPREATLELGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 112

RESULT 2  
ABB81749  
AC ABB81749;  
XX ABB81749;  
DT 10-SEP-2002 (first entry)  
XX  
DE Tumour necrosis factor receptor 1 death domain (shorter sequence).  
XX  
KW Tumour necrosis factor receptor 1; receptor; TNFR-1; death domain;  
KW receptor signalling; TNFR-1 DD; protein co-ordinate data.  
XX  
OS Unidentified.  
XX  
FH Key  
FT Region  
FT 15..21  
FT /label= Alpha\_helix\_1  
FT 28..34  
FT /label= Alpha\_helix\_2  
FT 38..42  
FT /label= Alpha\_helix\_3  
FT 52..65  
FT /label= Alpha\_helix\_4  
FT 72..85  
FT /label= Alpha\_helix\_5  
FT 89..98  
FT /label= Alpha\_helix\_6  
XX US2002045578-A1.  
XX  
PD 18-APR-2002.  
XX  
PF 14-MAY-2001; 2001US-00854906.  
XX  
PR 22-MAY-2000; 2000US-0206215P.  
XX  
PA (SUKI/) SUKITS S F.  
PA (XUGG/) XU G.  
PA (LINL/) LIN L.  
PA (TELL/) TELLIEZ J.  
PA (HSUS/) HSU S.  
XX  
XX Sukits SF, Xu G, Lin L, Telliez J, Hsu S;  
XX WPI; 2002-443412/47.  
XX  
XX Solution comprising tumor necrosis factor receptor 1 death domain, useful  
XX for identifying potential inhibitor of tumor necrosis factor receptor 1  
XX death domain.  
XX  
XX Claim 1; Fig 4; 49pp; English.  
XX  
XX The sequence represents the tumour necrosis factor receptor 1 death  
XX domain (TNFR-1 DD), which is the intracellular functional domain  
XX responsible for the receptor signalling activities. The invention relates  
XX to a novel solution comprising a tumour necrosis factor receptor 1 death  
XX domain. The solution is useful for identifying a potential inhibitor of

CC TNFR-1 DD, for the design and selection of potent and selective  
CC inhibitors of TNF signalling pathways, and for generating a three-  
CC dimensional structure for an unknown molecule or molecular complex  
XX Sequence 111 AA;

Query Match  
Best Local Similarity 98.6%; Score 579; DB 5; Length 111;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSM 61  
DB 1 AHKQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSM 60  
QY 62 ATWRRTPREATLELGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 112  
DB 61 ATWRRTPREATLELGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111

RESULT 3  
ABG70127  
ID ABG70127 standard; protein; 158 AA.  
XX  
AC ABG70127;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human prey protein for Shigella ipad #4.  
XX  
KW Prey protein; ospB; ospD; ipad; ipaC; ipaH9.8; ospG; ospC1; Shigella;  
KW shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid system;  
XX protein-protein interaction; SID; selected interacting domain; human.  
XX Homo sapiens.  
XX WO200257303-A2.  
XX 25-JUL-2002.  
XX  
PF 11-JAN-2002; 2002WO-EP000777.  
XX  
PR 12-JAN-2001; 2001US-0261130P.  
XX  
PA (HYBR-) HYBRIGENICS.  
XX  
PI Legrain P;  
XX  
DR WPI; 2002-599706/64.  
DR N-PSDB; ABS51520.  
XX  
XX New complex of protein-protein interactions between a bait Shigella  
XX flexneri polypeptide and a prey mammalian or human placenta polypeptide  
XX for treating or preventing bacillary dysentery in a mammal or human.  
XX Claim 7; Page 94; 162pp; English.  
XX  
XX The invention relates to a complex of protein-protein interactions  
XX between a Shigella flexneri polypeptide (e.g. ospB, ospD, ipad, ipaC,  
XX ipaH9.8, ospG and ospC1) and a mammalian polypeptide defined in the  
XX specification. The complexes are formed using the yeast two-hybrid  
XX system. Also included are (1) a recombinant host cell expressing the  
XX interactions between the Shigella flexneri polypeptide and a mammalian  
XX polypeptide defined in the specification; (2) selecting a modulating  
XX compound that inhibits or activates the protein-protein interactions;  
XX a modulating compound obtained from the method of (2); (4) a SID  
XX (selected interacting domain) polypeptide or its fragment or variant  
XX comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a  
XX SID polynucleotide or its fragment or variant comprising encoding the  
XX above polypeptides a vector comprising (5); (6) a recombinant host cell  
XX containing the vector; and (10) a protein chip comprising Shigella  
XX flexneri polypeptide and a mammalian polypeptide defined in the  
XX specification. A pharmaceutical composition comprising the compound,  
XX polypeptide or polynucleotide is useful for treating or preventing



CC shigellosis (bacillary dysentery) in a human or mammal. The present  
 CC sequence represents a human prey protein isolated by the yeast two-hybrid  
 CC assay, forming a complex of the invention with a shigella protein  
 XX  
 SQ Sequence 158 AA;

Query Match 98.6%; Score 579; DB 5; Length 158;  
 Best Local Similarity 99.1%; Pred. No. 1.5e-61;  
 Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKQSLDTPATLYAVENVPLRWKEFVKRLGLSDHEIDRLQLONGRCLEAQYSML 61  
 DB 48 AHKQSLDTPATLYAVENVPLRWKEFVKRLGLSDHEIDRLQLONGRCLEAQYSML 107  
 QY 62 ATWRRTPREATLELGRVLRMDLGLCLEDIEALCGPAALPPAPSLLR 112  
 DB 108 ATWRRTPREATLELGRVLRMDLGLCLEDIEALCGPAALPPAPSLLR 158

## RESULT 4

ABW00828  
 ID ABW00828 standard; protein; 426 AA.

XX AC ABW00828;

XX DT 15-JAN-2004 (first entry)

XX DE Human p55-R protein.

XX KW Intracellular domain; IC; p55 tumour necrotic factor receptor; TNF;  
 KW tumour; rheumatoid arthritis; inflammatory disease; gene therapy;  
 KW cytostatic; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Domain 206..426

FT /note= "p55 intracellular domain (IC)"

FT Domain 328..426

FT /note= "Death domain"

XX US6579697-B1.

XX 17-JUN-2003.

XX PF 12-NOV-1996; 96US-00747562.

XX PR 11-MAY-1995; 95WO-US005854.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Wallach D, Boldin M, Mett I, Varfolomeev E;

XX WPI; 2003-799831/75.

XX New DNA molecule encoding a polypeptide capable of binding to an  
 XX intracellular domain of a p55 tumor necrotic factor (TNF) receptor,  
 XX useful for preparing a composition for treating tumor, rheumatoid  
 XX arthritis or inflammatory diseases.

XX Claim 1; Col 101-104; 126pp; English.

XX The invention relates to an isolated DNA molecule which encodes a  
 CC polypeptide capable of binding to an intracellular domain of a p55 tumour  
 CC necrotic factor (TNF) receptor. The DNA molecule is useful for preparing  
 CC a composition for treating tumour, rheumatoid arthritis or inflammatory  
 CC diseases. The invention is useful in gene therapy. The present sequence  
 CC is the human p55IC-R protein

XX SQ Sequence 426 AA;

Query Match 98.6%; Score 579; DB 7; Length 426;  
 Best Local Similarity 99.1%; Pred. No. 5.4e-61;

Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 AHKQSLDTPATLYAVENVPLRWKEFVKRLGLSDHEIDRLQLONGRCLEAQYSML 61  
 DB 316 AHKQSLDTPATLYAVENVPLRWKEFVKRLGLSDHEIDRLQLONGRCLEAQYSML 375

QY 62 ATWRRTPREATLELGRVLRMDLGLCLEDIEALCGPAALPPAPSLLR 112

DB 376 ATWRRTPREATLELGRVLRMDLGLCLEDIEALCGPAALPPAPSLLR 426

## RESULT 5

AAB50895

ID AAB50895 standard; protein; 453 AA.

XX AC AAB50895;

XX DT 19-MAR-2001 (first entry)

XX DE Human TNFR 1.

XX KW Human; TR10 receptor; cytostatic; immunosuppressive; neuroprotective;  
 KW antiinflammatory; anti-HIV; antiparkinsonian; nootropic; cardiac;  
 KW vasotropic; antiallergic; antidiabetic; vulnary; ophthalmological;  
 KW antiviral; antibacterial; antifungal; antiparasitic; gene therapy; TNFR;  
 KW tumour necrosis factor receptor; cancer; leukaemia; autoimmune disorder;  
 KW apoptosis; cardiovascular disorder; inflammatory disease; wound;  
 KW infection; neurological disease; protein coordinate data.

XX OS Homo sapiens.

XX WO200073321-A1.

XX PD 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US014554.

XX PR 28-MAY-1999; 99US-0136786P.

XX PR 07-JUL-1999; 99US-0142563P.

XX PR 15-JUL-1999; 99US-0144023P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ni J;

XX WPI; 2001-025250/03.

XX Nucleic acid encoding a tumor necrosis factor receptor 10, useful in the  
 XX diagnosis, treatment or prevention of cancer, autoimmune disorders, and  
 XX diseases and disorders associated with apoptosis.

XX Disclosure; Fig 2; 212pp; English.

XX The present sequence is given in a specification relating to an isolated  
 CC nucleic acid encoding a human tumour necrosis factor receptor TR10. The  
 CC TR10 polynucleotide, polypeptide, antibodies, agonists and antagonists  
 CC are useful in the diagnosis, treatment or prevention of cancer, such as  
 CC breast and ovarian cancer and leukaemia; autoimmune disorders such as  
 CC multiple sclerosis, Crohn's disease and graft versus host disease;  
 CC diseases associated with increased apoptosis such as AIDS, Alzheimer's  
 CC disease and Parkinson's disease; cardiovascular disorders such as limb  
 CC ischaemia and congenital heart defects; inflammatory diseases e.g.  
 CC allergy; wound healing; disorders associated with neovascularisation,  
 CC e.g. diabetic retinopathy; infectious diseases such as viral, bacterial,  
 CC fungal and parasitic infections; and neurological diseases such as  
 CC amyotrophic lateral sclerosis

XX SQ Sequence 453 AA;

Query Match 98.6%; Score 579; DB 4; Length 453;

Best Local Similarity 99.1%; Pred. No. 5.8e-61;

Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKFEVKRLGLSDHEIDRLQLONGRCLEAQSML 61  
 Db |||||  
 QY 343 AHKPSLDTDDPATLYAVVENVPLRWKFEVKRLGLSDHEIDRLQLONGRCLEAQSML 402  
 Db |||||  
 QY 62 ATWRRTPRREATLELLGLRVLDMDLLGCLIEDIEALCGPAALPPAPSLIR 112  
 Db |||||  
 QY 403 ATWRRTPRREATLELLGLRVLDMDLLGCLIEDIEALCGPAALPPAPSLIR 453  
 |||||  
 RESULT 6  
 ABG74755  
 ID ABG74755 standard; protein; 455 AA.  
 AC ABG74755;  
 XX  
 DT 14-MAY-2003 (first entry)  
 XX  
 DE Human TNF-R protein huTNF-R.  
 XX  
 KW TNF; human; tumour necrosis factor; tumour necrosis factor receptor;  
 KW TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP393438-A.  
 XX  
 PD 24-OCT-1990.  
 XX  
 PF 06-APR-1990; 90EP-00106624.  
 XX  
 PR 21-APR-1989; 89DE-03913101.  
 PR 21-JUN-1989; 89DE-03920282.  
 XX  
 PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 PA (SYND ) SYNERGEN INC.  
 XX  
 PI Hauptmann R, Himmler A, Maurerfogy I, Stratowa C;  
 XX  
 DR WPI; 1990-321987/43.  
 DR N-PSDB; ABG77487.  
 XX  
 PT DNA encoding TNF binding protein and TNF-receptor - used in tumour  
 PT treatment and to understand mechanisms to TNF action.  
 PS Example 9; Fig 9; 51pp; German.  
 XX  
 CC This invention describes novel polynucleotide sequences encoding tumour  
 CC necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).  
 CC The products of the invention are useful in pharmaceutical compositions  
 CC for prophylaxis or treatment of human tumours and to understand the  
 CC mechanisms of TNF action. This sequence represents the huma TNF-R, huTNF-  
 CC R described in the disclosure of the invention  
 XX  
 SQ Sequence 455 AA;  
 Query Match 98.6%; Score 579; DB 2; Length 455;  
 Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
 Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 AHKPSLDTDDPATLYAVVENVPLRWKFEVKRLGLSDHEIDRLQLONGRCLEAQSML 61  
 Db |||||  
 QY 345 AHKPSLDTDDPATLYAVVENVPLRWKFEVKRLGLSDHEIDRLQLONGRCLEAQSML 404  
 Db |||||  
 QY 62 ATWRRTPRREATLELLGLRVLDMDLLGCLIEDIEALCGPAALPPAPSLIR 112  
 Db |||||  
 QY 405 ATWRRTPRREATLELLGLRVLDMDLLGCLIEDIEALCGPAALPPAPSLIR 455  
 |||||  
 RESULT 7  
 AAR07451  
 ID AAR07451 standard; protein; 455 AA.  
 XX  
 AC AAR07451;  
 XX

XX 25-MAR-2003 (revised)  
 DT 29-JAN-1991 (first entry)  
 XX  
 DE Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.  
 XX  
 KW Human tumour necrosis factor binding protein; TNF-BP; TNF-receptor;  
 KW infectious disease; parasitic disease; cachexia; autoimmune disease;  
 KW shock; lambdaTNF-R2; ratTNF-R8.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP393438-A.  
 XX  
 PD 24-OCT-1990.  
 XX  
 PF 06-APR-1990; 90EP-00106624.  
 XX  
 PR 21-APR-1989; 89DE-03913101.  
 PR 21-JUN-1989; 89DE-03920282.  
 XX  
 PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 PA (SYND ) SYNERGEN INC.  
 XX  
 PI Hauptmann R, Himmler A, Maurerfogy I, Stratowa C;  
 XX  
 DR WPI; 1990-321987/43.  
 DR N-PSDB; AAQ06285.  
 XX  
 PT DNA encoding TNF binding protein and TNF-receptor - used in tumour  
 PT treatment and to understand mechanisms to TNF action.  
 PS Disclosure; Fig 91(1-2); 51pp; German.  
 XX  
 CC ratTNF-R8 (AAQ06284) was used to screen the HS913T cDNA library. LambdaTNF  
 CC -R2 encodes the complete human TNF-R2 and was used to construct a plasmid  
 CC (pADTNF-R) expressing the product the same way as pADTNF-BP (see  
 CC AAQ06282). The expressed proteins are useful prophylactically and  
 CC therapeutically to control disorders which involve the damaging effects  
 CC of TNF-alpha or -beta (e.g. infectious or parasitic diseases, shock,  
 CC cachexia, autoimmune diseases, adult respiratory distress syndrome etc.,  
 CC or side effects of treatment with TNF-alpha). They can also be used as  
 CC diagnostic reagents for assaying TNF and in study of TNF-receptor  
 CC interactions. See also AAQ06282-Q06285. (Updated on 25-MAR-2003 to  
 CC correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 455 AA;  
 Query Match 98.6%; Score 579; DB 2; Length 455;  
 Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
 Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 AHKPSLDTDDPATLYAVVENVPLRWKFEVKRLGLSDHEIDRLQLONGRCLEAQSML 61  
 Db |||||  
 QY 345 AHKPSLDTDDPATLYAVVENVPLRWKFEVKRLGLSDHEIDRLQLONGRCLEAQSML 404  
 Db |||||  
 QY 62 ATWRRTPRREATLELLGLRVLDMDLLGCLIEDIEALCGPAALPPAPSLIR 112  
 Db |||||  
 QY 405 ATWRRTPRREATLELLGLRVLDMDLLGCLIEDIEALCGPAALPPAPSLIR 455  
 |||||  
 RESULT 8  
 ABG74751  
 ID ABG74751 standard; protein; 455 AA.  
 XX  
 AC ABG74751;  
 XX  
 DT 14-MAY-2003 (first entry)  
 XX  
 DE Human TNF receptor protein.  
 XX  
 KW TNF; human; tumour necrosis factor; tumour necrosis factor receptor;  
 KW TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.

```

XX OS Homo sapiens.
XX PN EP393438-A.
XX PD 24-OCT-1990.
XX PF 06-APR-1990; 90EP-00106624.
XX PR 21-APR-1989; 89DE-03913101.
XX PR 21-JUN-1989; 89DE-03920282.
XX PA (BOEH ) BOHRINGER INGELHEIM INT GMBH.
XX PA (SYND ) SYNERGEN INC.
XX PI Hauptmann R, Himmeler A, Maurerfogy I, Stratowa C;
XX DR WPI; 1990-321987/43.
XX FT DNA encoding TNF binding protein and TNF- receptor - used in tumour
XX PT treatment and to understand mechanisms to TNF action.
XX PS Claim 22; Page 34; 51pp; German.
XX CC This invention describes novel polynucleotide sequences encoding tumour
XX CC necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).
XX CC The products of the invention are useful in pharmaceutical compositions
XX CC for prophylaxis or treatment of human tumours and to understand the
XX CC mechanisms of TNF action. This sequence represents the TNF receptor
XX CC described in the disclosure of the invention
XX SQ Sequence 455 AA;

Query Match 98.6%; Score 579; DB 2; Length 455;
Best Local Similarity 99.1%; Pred. No. 5.9e-61;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSQSLDTPATLYAVVENVPPPLRWKEFVKRLGLSDHEIDRLQLONGRCICREAYQSM 61
Db 345 AHKPSQSLDTPATLYAVVENVPPPLRWKEFVKRLGLSDHEIDRLQLONGRCICREAYQSM 404
QY 62 ATWRRRTPRREATLELGRVLRDMDLLGCLDIEEALCGPALPPAPSLR 112
Db 405 ATWRRRTPRREATLELGRVLRDMDLLGCLDIEEALCGPALPPAPSLR 455

RESULT 9
AAR12550
ID AAR12550 standard; protein; 455 AA.
XX AC AAR12550;
XX DT 25-MAR-2003 (revised)
XX DT 12-SEP-1991 (first entry)
XX DE Type I TNF receptor.
XX KW Tumour Necrosis Factor; TNF; binding protein; TBP-I.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..21 /label= sig_peptide
XX FT Domain 21..203 /label= soluble_domain
XX FT /note= "may be 2 amino acids shorter or contain a few
XX FT additional amino acids"
XX FT Protein 22..455 /label= mat_protein
XX FT 41..53 /label= TBP-I derived sequence
XX FT Region 44..83
XX FT Region

```

```

FT Modified-site /label= repeat_1
FT 54..56 /label= N-glycosylation_site
FT Region 84..126 /label= repeat_2
FT Region 110..124 /label= TBP-I derived sequence
FT Region 127..167 /label= repeat_3
FT Modified-site 145..147 /label= N-glycosylation_site
FT Modified-site 151..153 /label= N-glycosylation_site
FT Region 168..201 /label= repeat_4
FT Region 199..201 /label= TBP-I derived sequence
FT Domain 212..234 /label= transmembrane_domain
FT PN EP433900-A.
XX PD 26-JUN-1991.
XX PF 13-DEC-1990; 90EP-00124133.
XX PR 13-DEC-1989; 89IL-00092697.
XX PR 12-JUL-1990; 90IL-00095064.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PA (WALL/) WALLACH D.
XX PI Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
XX PI Aderka D;
XX DR WPI; 1991-186774/26.
XX DR N-PSDB; AAQ12215.
XX PT Recombinant tumour necrosis factor binding protein I - prepd. by
XX PT transfecting eukaryotic cells with vector contg. deoxyribonucleic acid
XX PT encoding human type I TNF receptor or soluble domain.
XX PS Disclosure; Fig 1(D); 30pp; English.
XX CC The Tumour Necrosis Factor Binding Protein I is the soluble form of type
XX CC I TNF-receptor and constitutes a fragment of the cell surface form of
XX CC this receptor, corresp. to its extracellular domain. The soluble proteins
XX CC produced by the transfected cells secreted into the medium may have at
XX CC the N-terminus the sequence Asp-Ser-Val (41-43), or the sequence Leu-Val-
XX CC Pro (30-32) or Ile-Tyr-Pro (22-24) or any other sequence between Ile (21)
XX CC and Asp (41). See also AAQ12212-15. (Updated on 25-MAR-2003 to correct PA
XX CC field.)
XX SQ Sequence 455 AA;

Query Match 98.6%; Score 579; DB 2; Length 455;
Best Local Similarity 99.1%; Pred. No. 5.9e-61;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSQSLDTPATLYAVVENVPPPLRWKEFVKRLGLSDHEIDRLQLONGRCICREAYQSM 61
Db 345 AHKPSQSLDTPATLYAVVENVPPPLRWKEFVKRLGLSDHEIDRLQLONGRCICREAYQSM 404
QY 62 ATWRRRTPRREATLELGRVLRDMDLLGCLDIEEALCGPALPPAPSLR 112
Db 405 ATWRRRTPRREATLELGRVLRDMDLLGCLDIEEALCGPALPPAPSLR 455

RESULT 10
AAR10986
ID AAR10986 standard; protein; 455 AA.
XX AC AAR10986;

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XX 25-MAR-2003 (revised)  
 DT 13-MAY-1991 (first entry)  
 XX 30kD TNF inhibitor precursor.  
 DE Tumour necrosis factor; inhibitor.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT Cleavage-site 40..41  
 FT /note= " cleavage gives active protein "  
 XX AU9058976-A.  
 XX 24-JAN-1991.  
 XX 16-JUL-1990; 90AU-00058976.  
 XX 18-JUL-1989; 89US-00381080.  
 PR 11-DEC-1989; 89US-00450329.  
 PR 07-FEB-1990; 90US-00479661.  
 XX (SYND ) SYNERGEN INC.  
 XX WPI; 1991-073847/11.  
 DR N-PSDB; AAQ10883.  
 XX Tumour necrosis factor inhibitor - for suppression of tnfr-alpha and -  
 PT beta, useful as therapeutic agent.  
 XX Disclosure; Fig 21; 142pp; English.  
 XX The sequence comprises the entire 30 kD TNF inhibitor. The clone from  
 CC which the sequence was deduced was isolated from a cDNA library prep'd.  
 CC from RNA form U937 cells treated with PMA/PHA. The whole gene can be  
 CC inserted into expression vectors for prep'n of TNF inhibitor for use in  
 CC the treatment of inflammatory and degenerative diseases. The active  
 CC protein is claimed (Claim 8). See also AAR10984 and AAR11001. (Updated on  
 CC 25-MAR-2003 to correct PA field.)  
 XX Sequence 455 AA;  
 SQ  
 Query Match 98.6%; Score 579; DB 2; Length 455;  
 Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
 Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 AHKPSLDTDDPATLYAVVENVPLRWKFEVRLGLSDHEIDRLQNGRCLEAQYSML 61  
 Db 345 AHKPSLDTDDPATLYAVVENVPLRWKFEVRLGLSDHEIDRLQNGRCLEAQYSML 404  
 Qy 62 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 112  
 Db 405 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455  
 RESULT 11  
 AAR11082  
 ID AAR11082 standard; protein; 455 AA.  
 XX AAR11082;  
 AC  
 XX 09-JAN-2003 (revised)  
 DT 24-MAY-1991 (first entry)  
 DE Human 55kD TNF-binding protein.  
 XX Tumour Necrosis Factor; binding proteins; septic shock;  
 KW autoimmune glomerulonephritis; lymphokine; cytokine.  
 XX Homo sapiens.

PH Key Location/Qualifiers  
 FT Peptide 1..28  
 FT /label= signal peptide  
 FT Modified-site 54  
 FT Modified-site /label= putative N-glycosylation site  
 FT Modified-site 145  
 FT Modified-site /label= putative N-glycosylation site  
 FT Modified-site 151  
 FT Region /label= putative N-glycosylation site  
 FT 212..230  
 FT /label= transmembrane region  
 FT Modified-site 270  
 FT /label= putative N-glycosylation site  
 XX EP417563-A.  
 XX 20-MAR-1991.  
 XX 31-AUG-1990; 90EP-00116707.  
 XX 12-SEP-1989; 89CH-00003319.  
 PR 08-MAR-1990; 90CH-00000746.  
 PR 20-APR-1990; 90CH-00001347.  
 XX (HOFF ) HOFFMANN-LA ROCHE AG.  
 XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;  
 PI Schlaeger EJ;  
 XX WPI; 1991-081851/12.  
 DR N-PSDB; AAQ10955.  
 XX Insoluble tumour necrosis factor binding proteins - and DNA encoding  
 PT them, useful in pharmaceutical prods. and for antibody prodn.  
 XX Claim 1; Fig 1; 26pp; German.  
 XX Partial amino acid sequences were determined for the 55 and 75kD TNF-BPs  
 CC (see AAR11072-R11081) and oligonucleotide primers were synthesised based  
 CC on these partial sequences. The primers were used to produce a cDNA  
 CC fragment for use as a probe to screen a human placental cDNA bank  
 CC constructed in lambda gt11. Positive clones were identified and sequenced.  
 CC DNA constructs comprising the TNF-BP coding sequence may also contain a  
 CC fragment encoding a human Ig domain. Recombinant constructs are used to  
 CC transform cells to confer improved TNF-binding properties. See also  
 CC AAQ10956. (Updated on 09-JAN-2003 to add missing QS field.)  
 XX Sequence 455 AA;  
 SQ  
 Query Match 98.6%; Score 579; DB 2; Length 455;  
 Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
 Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 AHKPSLDTDDPATLYAVVENVPLRWKFEVRLGLSDHEIDRLQNGRCLEAQYSML 61  
 Db 345 AHKPSLDTDDPATLYAVVENVPLRWKFEVRLGLSDHEIDRLQNGRCLEAQYSML 404  
 Qy 62 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 112  
 Db 405 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455  
 RESULT 12  
 AAR20787  
 ID AAR20787 standard; protein; 455 AA.  
 XX AAR20787;  
 AC  
 XX 11-MAY-1992 (first entry)  
 DT TNF-alpha binding protein.  
 DE Tumour necrosis factor alpha; autoimmune diseases; cachectin;  
 XX KW

KW	Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW	IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW	rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW	pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW	graft versus host disease; sepsis; inflammation; allergy;
KW	autoimmune dysfunction.
XX	
OS	Homo sapiens.
OS	Bacteriophage lambda.
XX	
Key	Location/Qualifiers
FT	Peptide
FT	1..40
FT	/note= "signal peptide"
FT	41..455
FT	/note= "Mature hTNF-R"
FT	
XX	
XX	W09319777-A1.
PN	
XX	
XX	
PD	14-OCT-1993.
XX	
XX	
XX	26-MAR-1993; 93WO-US002938.
XX	
PR	30-MAR-1992; 92US-00860710.
XX	
XX	(TMV ) IMMUNEX CORP.
PA	
XX	Smith CA;
PI	
XX	
XX	WPI; 1993-336592/42.
DR	
DR	N-PSDB; AAQ49932.
DR	
XX	
PT	New fusion protein tumour necrosis factor and human interleukin-1
PT	receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid
PT	arthritis, diabetes, cerebral malaria, sepsis, etc.
XX	
PS	Disclosure; Page 57-59; 85pp; English.
XX	
CC	The sequences given in AAR42058-59 represent human tumour necrosis
CC	factor receptor (TNF-R) and the sequences in AAR42060-61 represent human
CC	interleukin-1 receptor (IL-1R). These sequences were used in the
CC	production of a fusion protein which conformed to one of the formulae:
CC	TNF-R-linker-TNF-R-linker-IL-1R IL-1R-linker-TNF-R-linker-TNF-R or TNF-R-
CC	linker-TNF-R The linker may comprise 5-100 amino acids selected from Gly,
CC	Asp, Ser, Thr and Ala. These linkers separate the individual moieties by
CC	such a distance that each component of the fusion protein is capable of
CC	folding into the secondary or tertiary structure required for its
CC	biological activity. These fusion proteins may be used in therapy,
CC	in conditions in which both TNF and IL-1 play a causative role. They may
CC	be used to treat cachexia, rheumatoid arthritis, diabetes, multiple
CC	sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft
CC	and xenograft rejection in graft versus host disease, sepsis, septic
CC	shock, inflammation, allergies and autoimmune dysfunctions. (Updated on
CC	25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS
CC	field.)
XX	
SQ	Sequence 455 AA;
	Query Match 98.6%; Score 579; DB 2; Length 455;
	Best Local Similarity 99.1%; Pred. No. 5.9e-61;
	Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	2 AHKQPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCRLREAQYSML 61
Db	345 AHKQPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCRLREAQYSML 404
Qy	62 ATWRRTPREATLELLGRVLRMDMLGCLDEBEALCGPAALPPAPSLLR 112
Db	405 ATWRRTPREATLELLGRVLRMDMLGCLDEBEALCGPAALPPAPSLLR 455

RESULT 14  
AAR51034

ID AAR51034 standard; protein; 455 AA.  
 AC AAR51034;  
 XX  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 13-MAY-1994 (first entry)  
 XX  
 DE Mutant p55 tumour necrosis factor receptor.  
 XX  
 XX  
 KW TNF; tumour necrosis factor; receptor; disease; autoimmunity;  
 KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;  
 KW effector protein.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1. .21  
 FT /label= Leader peptide.  
 FT Domain 183. .205  
 FT /label= Transmembrane domain.  
 XX  
 PN EP568925-A2.  
 XX  
 XX  
 PD 10-NOV-1993.  
 XX  
 XX  
 PF 29-APR-1993; 93EP-00106981.  
 XX  
 PR 03-MAY-1992; 92IL-00101769.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Wallach D, Brakebusch C;  
 XX  
 DR WPI; 1993-353057/45.  
 DR N-PSDB; AAQ50870.  
 XX  
 PT Modulating activity of tumour necrosis factor receptor - using  
 PT peptide(s), antibodies, etc. which interact with critical regions of  
 PT receptor or effector protein, for controlling auto-immune disease, septic  
 PT shock, etc.  
 XX  
 PS Claim 5; Fig 1; 17pp; English.  
 XX  
 CC Modification of the tumour necrosis factor receptor by mutation or  
 CC deletion modulates signal transduction and/or cleavage effected by the  
 CC receptor. This modulation of activity can also be achieved using effector  
 CC proteins which interact with the TNF receptor. Molecules which interact  
 CC with the TNF receptor or the effector proteins can be used to treat or  
 CC prevent diseases associated with TNF activity e.g. autoimmune disease;  
 CC rheumatoid arthritis; graft rejection; graft vs. host disease or septic  
 CC shock. They can also be used to treat overdoses of exogenous TNF.  
 CC Specific deletions include amino acid residues 405-426 from which it was  
 CC discovered that amino acids 405-414, or part of them, are essential for  
 CC the signalling of the human p55 TNF-R for the cytotoxic effect of TNF  
 CC whereas amino acids 415-426 are not essential. Also residues 170-174, 174  
 CC -179 or both i.e 170-179 were deleted. This region of amino acids, or  
 CC part of, when deleted, abolished shedding of the soluble extracellular  
 CC forms of the protein. This sequence corresponds to the wild type protein  
 CC disclosed in AAR42197 except that alanine at position 197 has been  
 CC substituted in place of serine. The substitution inhibits cleavage of the  
 CC soluble form of the protein. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 455 AA;

Query Match 98.6%; Score 579; DB 2; Length 455;  
 Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
 Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 2 AHKPSLTDTPATLYAVVENPPLRWKFEVRLGLSDHEIDRLQNGRCLEAQYSML 61  
 345 AHKPSLTDTPATLYAVVENPPLRWKFEVRLGLSDHEIDRLQNGRCLEAQYSML 404

Query Match 98.6%; Score 579; DB 2; Length 455;  
 Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
 Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 2 AHKPSLTDTPATLYAVVENPPLRWKFEVRLGLSDHEIDRLQNGRCLEAQYSML 61  
 345 AHKPSLTDTPATLYAVVENPPLRWKFEVRLGLSDHEIDRLQNGRCLEAQYSML 404

QY 62 ATWRRTPRRATLELLGRVLRDMDLLGCLIEDIEALCGPALPPAPSLR 112  
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 Db 405 ATWRRTPRRATLELLGRVLRDMDLLGCLIEDIEALCGPALPPAPSLR 455  
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 AAR42197  
 ID AAR42197 standard; protein; 455 AA.  
 AC AAR42197;  
 XX  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 13-MAY-1994 (first entry)  
 XX  
 XX  
 DE p55 Tumour necrosis factor receptor.  
 XX  
 XX  
 KW TNF; tumour necrosis factor; receptor; disease; autoimmunity;  
 KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;  
 KW effector protein.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1. .21  
 FT /label= Leader peptide.  
 FT Domain 183. .205  
 FT /label= Transmembrane domain.  
 XX  
 PN EP568925-A2.  
 XX  
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 PD 10-NOV-1993.  
 XX  
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 PF 29-APR-1993; 93EP-00106981.  
 XX  
 PR 03-MAY-1992; 92IL-00101769.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Wallach D, Brakebusch C;  
 XX  
 DR WPI; 1993-353057/45.  
 DR N-PSDB; AAQ50870.  
 XX  
 PT Modulating activity of tumour necrosis factor receptor - using  
 PT peptide(s), antibodies, etc. which interact with critical regions of  
 PT receptor or effector protein, for controlling auto-immune disease, septic  
 PT shock, etc.  
 XX  
 PS Claim 2; Fig 1; 17pp; English.  
 XX  
 CC Modification of the tumour necrosis factor receptor by mutation or  
 CC deletion modulates signal transduction and/or cleavage effected by the  
 CC receptor. This modulation of activity can also be achieved using effector  
 CC proteins which interact with the TNF receptor. Molecules which interact  
 CC with the TNF receptor or the effector proteins can be used to treat or  
 CC prevent diseases associated with TNF activity e.g. autoimmune disease;  
 CC rheumatoid arthritis; graft rejection; graft vs. host disease or septic  
 CC shock. They can also be used to treat overdoses of exogenous TNF.  
 CC Specific deletions include amino acid residues 405-426 from which it was  
 CC discovered that amino acids 405-414, or part of them, are essential for  
 CC the signalling of the human p55 TNF-R for the cytotoxic effect of TNF  
 CC whereas amino acids 415-426 are not essential. Also residues 170-174, 174  
 CC -179 or both i.e 170-179 were deleted. This region of amino acids, or  
 CC part of, when deleted, abolished shedding of the soluble extracellular  
 CC forms of the protein. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 455 AA;

Query Match 98.6%; Score 579; DB 2; Length 455;  
 Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
 Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 2 AHKPSLTDTPATLYAVVENPPLRWKFEVRLGLSDHEIDRLQNGRCLEAQYSML 61

Db 345 AHKQSLDDEATLYAVVENVPLRWKEFVRRGLSDHEIDRLQNGRCLREBAQYSML 404  
Qy 62 ATWRRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db 405 ATWRRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455

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Job time : 50.9581 secs

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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:41:22 ; Search time 14.0838 Seconds  
(without alignments)  
410.549 Million cell updates/sec

Title: US-09-854-906-1

Perfect score: 587

Sequence: 1 MAHKPQSLDTPATLYAVV.....DIEEALCGPAALPPAPSLLR 112

Scoring table: BLOSUM62

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents AA.\*

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4: /cgm2\_6/ptodata/2/iaa/6B\_COMB.pep.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	579	98.6	453	3	US-09-086-483A-5
3	579	98.6	453	4	US-09-580-212-5
4	579	98.6	453	4	US-09-769-402-5
5	579	98.6	455	1	US-08-321-668-2
6	579	98.6	455	1	US-08-837-941-2
7	579	98.6	455	2	US-08-126-016-2
8	579	98.6	455	3	US-08-815-469-5
9	579	98.6	455	3	US-09-006-353A-3
10	579	98.6	455	4	US-09-527-236A-5
11	579	98.6	455	4	US-08-054-970-2
12	579	98.6	455	4	US-09-565-918-4
13	579	98.6	455	4	US-09-573-986-3
14	579	98.6	455	4	US-09-027-287-3
15	579	98.6	455	4	US-09-252-656B-3
16	579	98.6	455	4	US-08-406-824A-4
17	579	98.6	455	4	US-09-523-323-3
18	579	98.6	455	4	US-09-756-854-5
19	579	98.6	909	4	US-09-013-895A-4
20	579	98.6	909	4	US-09-448-868-4
21	574	97.8	455	1	US-08-050-319B-25
22	574	97.8	455	2	US-08-465-982-25
23	443	75.5	86	3	US-09-042-785A-25
24	443	75.5	108	2	US-08-580-988A-20
25	421	71.7	471	4	US-09-513-007-2
26	404	68.8	78	4	US-08-828-683A-23
27	394.5	67.2	84	4	US-09-069-827A-120

Sequence 6, Appli  
Sequence 23, Appl  
Sequence 23, Appl  
Sequence 3, Appli  
Sequence 11, Appl  
Sequence 29, Appl  
Sequence 23, Appl  
Sequence 28, Appl  
Sequence 35, Appl  
Sequence 5, Appli  
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Sequence 5, Appli  
Sequence 10, Appl  
Sequence 6, Appli  
Sequence 2, Appli  
Sequence 24, Appl

#### ALIGNMENTS

RESULT 1

US-08-747-562-37

; Sequence 37, Application US/08747562

; Patent No. 6579697

; GENERAL INFORMATION:

; APPLICANT: WALLACH, David

; APPLICANT: BOLDIN, Mark

; APPLICANT: METT, Igor

; APPLICANT: VARFOLOMEEV, Eugene

; TITLE OF INVENTION: MODULATOR OF TNF/NGF SUPERFAMILY RECEPTORS

; TITLE OF INVENTION: AND SOLUBLE OLIGOMERIC TNF/NGF SUPERFAMILY RECEPTORS

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/08/747,562

; APPLICATION NUMBER: PCT/US95/05854

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 111,125

; FILING DATE: 02-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: WALLACH=15A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 426 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-747-562-37



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Query Match      98.6%; Score 579; DB 4; Length 426;
Best Local Similarity 99.1%; Pred. No. 4.2e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      316 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAQYSML 375
      |||||

Qy      62 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112
      |||||
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RESULT 2
US-09-086-483A-5
; Sequence 5, Application US/09086483A
; Patent No. 6214580
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/086,483A
; FILING DATE: May-29-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,936
; FILING DATE: May-30-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/069,112
; FILING DATE: Dec-9-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-086-483A-5

Query Match      98.6%; Score 579; DB 3; Length 453;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAQYSML 61
      |||||
Db      343 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAQYSML 402
      |||||

Qy      62 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112
      |||||
Db      403 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 453
      |||||
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RESULT 3
US-09-580-212-5
; Sequence 5, Application US/09580212
; Patent No. 6506569
; GENERAL INFORMATION:
; APPLICANT: NI, Jian et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR10
; FILE REFERENCE: PF379PL
; CURRENT APPLICATION NUMBER: US/09/580,212
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,786
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,563
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/144,023
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-580-212-5

Query Match      98.6%; Score 579; DB 4; Length 453;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAQYSML 61
      |||||
Db      343 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAQYSML 402
      |||||

Qy      62 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112
      |||||
Db      403 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 453
      |||||

RESULT 4
US-09-769-402-5
; Sequence 5, Application US/09769402
; Patent No. 6607726
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/769,402
; FILING DATE: 26-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/086,483
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 60/069,112
; FILING DATE: Dec-9-97
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF379
; TELECOMMUNICATION INFORMATION:
```

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/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8439
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 453 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-769-402-5

Query Match          98.6%; Score 579; DB 4; Length 453;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSL 61
Db 343 AHKQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSL 402
QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112
Db 403 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 453

RESULT 5
US-08-321-668-2
/ Sequence 2, Application US/08321668
/ Patent No. 5665859
/ GENERAL INFORMATION:
/ APPLICANT: WALLACH, David
/ APPLICANT: BRAKEBUSCH, Cord
/ APPLICANT: VARFOLOMEEV, Eugene
/ APPLICANT: BATKIN, Michael
/ TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
/ TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/321,668
/ FILING DATE: 12-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IL 107268
/ FILING DATE: 12-OCT-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: WALLACH=13
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 455 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-321-668-2

Query Match          98.6%; Score 579; DB 1; Length 455;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSL 61
Db 343 AHKQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSL 404
QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112
Db 405 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455
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Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSL 61
Db 345 AHKQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSL 404
QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112
Db 405 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 6
US-08-837-941-2
/ Sequence 2, Application US/08837941
/ Patent No. 5766917
/ GENERAL INFORMATION:
/ APPLICANT: WALLACH, David
/ APPLICANT: BRAKEBUSCH, Cord
/ APPLICANT: VARFOLOMEEV, Eugene
/ APPLICANT: BATKIN, Michael
/ TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
/ TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/837,941
/ FILING DATE: 28-APR-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/321,668
/ FILING DATE: 12-OCT-1994
/ APPLICATION NUMBER: IL 107268
/ FILING DATE: 12-OCT-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: WALLACH=13
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 455 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-837-941-2

Query Match          98.6%; Score 579; DB 1; Length 455;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSL 61
Db 345 AHKQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSL 404
QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112
Db 405 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455
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RESULT 7  
US-08-126-016-2  
; Sequence 2, Application US/08126016  
; Patent No. 5811261  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, DAVID  
; APPLICANT: NOHAR, YARON  
; APPLICANT: KEMPER, OLIVER  
; APPLICANT: ENGELMANN, HARTMUT  
; APPLICANT: BRAKEBUSCH, CORD  
; APPLICANT: ADEKA, DAN  
; TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR  
; TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/126,016  
; FILING DATE: 24-SEP-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/625668  
; FILING DATE: 13-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, ROGER L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-126-016-2

Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 AHKPSLDTDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLONGRCLEAQSML 61  
DB 345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLONGRCLEAQSML 404  
  
QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
DB 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 8  
US-08-815-469-5  
; Sequence 5, Application US/08815469  
; Patent No. 6153402  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.

; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,469  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 6153402 Yet Assigned  
; FILING DATE: 06-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/028,711  
; FILING DATE: 17-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/013,285  
; FILING DATE: 12-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
US-08-815-469-5

Query Match 98.6%; Score 579; DB 3; Length 455;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 AHKPSLDTDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLONGRCLEAQSML 61  
DB 345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLONGRCLEAQSML 404  
  
QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
DB 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 9  
US-09-006-353A-3  
; Sequence 3, Application US/09006353A  
; Patent No. 6261801  
; GENERAL INFORMATION:  
; APPLICANT: WEI, YING-FEI  
; APPLICANT: YU, GUO-LIANG  
; APPLICANT: GENTZ, REINER  
; APPLICANT: RUBEN, STEVEN  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US

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; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-006-353A-3

Query Match 98.6%; Score 579; DB 3; Length 455;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVNPPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 61
Db 345 AHKPSLDTDDPATLYAVVNPPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 404

QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLIEDIEALCGPAALPPAPSLR 112
Db 405 ATWRRTPREATLELLGRVLRDMDLLGCLIEDIEALCGPAALPPAPSLR 455

RESULT 10
US-09-527-236A-5
; Sequence 5, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-527-236A-5

Query Match 98.6%; Score 579; DB 4; Length 455;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVNPPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 61
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Db 345 AHKPSLDTDDPATLYAVVNPPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 404

QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLIEDIEALCGPAALPPAPSLR 112
Db 405 ATWRRTPREATLELLGRVLRDMDLLGCLIEDIEALCGPAALPPAPSLR 455

RESULT 11
US-08-054-970-2
; Sequence 2, Application US/08054970
; Patent No. 6395267
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/054,970
; FILING DATE: 03-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-054-970-2

Query Match 98.6%; Score 579; DB 4; Length 455;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVNPPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 61
Db 345 AHKPSLDTDDPATLYAVVNPPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 404

QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLIEDIEALCGPAALPPAPSLR 112
Db 405 ATWRRTPREATLELLGRVLRDMDLLGCLIEDIEALCGPAALPPAPSLR 455

RESULT 12
US-09-565-918-4
; Sequence 4, Application US/09565918
; Patent No. 6433147
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
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; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/09/565,918
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-565-918-4

Query Match      98.6%; Score 579; DB 4; Length 455;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 61
DB 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 404

QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 112
DB 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 13
US-09-573-986-3
; Sequence 3, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-573-986-3

Query Match      98.6%; Score 579; DB 4; Length 455;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 61
DB 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 404

QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 112
DB 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 14
US-09-027-287-3
; Sequence 3, Application US/09027287A
; Patent No. 6479254
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; US-09-027-287-3

Query Match      98.6%; Score 579; DB 4; Length 455;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 61
DB 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 404

QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 112
DB 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 15
US-09-252-656B-3
; Sequence 3, Application US/09252656B
; Patent No. 6495520
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Zhang, Jun
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1486.0650006
; CURRENT APPLICATION NUMBER: US/09/252,656B
; CURRENT FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 60/075,409
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/027,287
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/003,886
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 08/822,953
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/013,923
; PRIOR FILING DATE: 1996-03-22
; PRIOR APPLICATION NUMBER: US 60/030,157
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-252-656B-3

Query Match      98.6%; Score 579; DB 4; Length 455;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 61
DB 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQYSML 404

QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 112
DB 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 455
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Qy	2	AHKQSDLTDDPATLYAVENVPPRLRWKEFKVRLGLSDHEIDELQNGRCRLRAEQYSML	61
Db	345	AHKQSDLTDDPATLYAVENVPPRLRWKEFKVRLGLSDHEIDELQNGRCRLRAEQYSML	404
Qy	62	ATWRRTPRREATLELGRVLDRMDLLGCLDIEEALCGPAALPAPSLLR	112
Db	405	ATWRRTPRREATLELGRVLDRMDLLGCLDIEEALCGPAALPAPSLLR	455

Search completed: June 1, 2004, 14:48:03  
Job time : 15.0838 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	579	98.6	158	14	US-10-043-487-301	Sequence 301, Appl
2	579	98.6	426	15	US-10-349-977-37	Sequence 37, Appl
3	579	98.6	453	14	US-10-280-047-5	Sequence 5, Appl
4	579	98.6	455	9	US-09-836-212-3	Sequence 3, Appl
5	579	98.6	455	9	US-09-333-966-5	Sequence 5, Appl
6	579	98.6	455	9	US-09-027-287-3	Sequence 3, Appl
7	579	98.6	455	9	US-09-874-138-3	Sequence 3, Appl
8	579	98.6	455	9	US-09-840-707A-16	Sequence 16, Appl
9	579	98.6	455	9	US-09-232-656B-3	Sequence 3, Appl
10	579	98.6	455	9	US-09-839-422-2	Sequence 2, Appl
11	579	98.6	455	9	US-09-899-422-17	Sequence 17, Appl
12	579	98.6	455	9	US-09-935-727-5	Sequence 5, Appl
13	579	98.6	455	9	US-09-898-234-2	Sequence 2, Appl
14	579	98.6	455	9	US-09-898-234-17	Sequence 17, Appl
15	579	98.6	455	9	US-09-756-854-5	Sequence 5, Appl





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/ Patent No. US20020009773A1
/ GENERAL INFORMATION:
/ APPLICANT: Yu, Guo-Liang
/ APPLICANT: Ni, Jian
/ APPLICANT: Dixit, Vishva L.
/ APPLICANT: Gentz, Reiner L.
/ APPLICANT: Dillon, Patrick J.
/ TITLE OF INVENTION: Death Domain Containing Receptors
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
/ STREET: 1100 New York Ave., NW, Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/333,966
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/815,469
/ FILING DATE:
/ APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
/ FILING DATE: 06-FEB-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/028,711
/ FILING DATE: 17-OCT-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/013,285
/ FILING DATE: 12-MAR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Steffe, Eric K.
/ REGISTRATION NUMBER: 36,688
/ REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 455 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: No. US20020009773A1 Relevant
/ TOPOLOGY: No. US20020009773A1 Relevant
/ MOLECULE TYPE: protein
/ US-09-333-966-5

Query Match 98.6%; Score 579; DB 9; Length 455;
Best Local Similarity 99.1%; Pred. No. 1.3e-57;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSQLDTPATLYAVVENVPPLEKGFVKRLGSDHEIDRLQNGRCLEAQYSML 61
Db 345 AHKPSQLDTPATLYAVVENVPPLEKGFVKRLGSDHEIDRLQNGRCLEAQYSML 404

QY 62 ATWRRTPREATLELLGRVLRDMLGCLDIEEALCGPAALPPAPSLLR 112
Db 405 ATWRRTPREATLELLGRVLRDMLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 7
US-09-874-138-3
/ Sequence 3, Application US/09874138
/ Patent No. US20020072091A1
/ GENERAL INFORMATION:
/ APPLICANT: Ni, Jian
/ APPLICANT: Gentz, Reiner L.
/ APPLICANT: Yu, Guo-liang
/ APPLICANT: Rosen, Craig A.
/ TITLE OF INVENTION: Death Domain Containing Receptor 5
/ FILE REFERENCE: 1488.1310006
/ CURRENT APPLICATION NUMBER: US/09/874,138
/ CURRENT FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 09/565,009
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: 60/148,939
/ PRIOR FILING DATE: 1999-08-13
/ PRIOR APPLICATION NUMBER: 60/133,238
/ PRIOR FILING DATE: 1999-05-07
/ PRIOR APPLICATION NUMBER: 60/132,498
/ PRIOR FILING DATE: 1999-05-04
/ PRIOR APPLICATION NUMBER: 09/042,583
/ PRIOR FILING DATE: 1998-03-17
/ PRIOR APPLICATION NUMBER: 60/054,021
/ PRIOR FILING DATE: 1997-07-29
/ PRIOR APPLICATION NUMBER: 60/040,846
/ PRIOR FILING DATE: 1997-03-17
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 455
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-874-138-3

Query Match 98.6%; Score 579; DB 9; Length 455;
Best Local Similarity 99.1%; Pred. No. 1.3e-57;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSQLDTPATLYAVVENVPPLEKGFVKRLGSDHEIDRLQNGRCLEAQYSML 61
Db 345 AHKPSQLDTPATLYAVVENVPPLEKGFVKRLGSDHEIDRLQNGRCLEAQYSML 404

QY 62 ATWRRTPREATLELLGRVLRDMLGCLDIEEALCGPAALPPAPSLLR 112
Db 405 ATWRRTPREATLELLGRVLRDMLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 6
US-09-027-287-3
/ Sequence 3, Application US/09027287A
/ Patent No. US20020064869A1
/ GENERAL INFORMATION:
/ APPLICANT: Ebner, Reinhard
/ APPLICANT: Yu, Guo-Liang
/ APPLICANT: Ruben, Steven M.
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QY 2 AHKQSLDTPATLYAVVENPPLRWKKEFVKRLGLSDHEIDRLQLONGRCCLREAYQY 61  
DB 345 AHKQSLDTPATLYAVVENPPLRWKKEFVKRLGLSDHEIDRLQLONGRCCLREAYQY 404  
QY 62 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
DB 405 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

## RESULT 8

US-09-840-707A-16  
; Sequence 16, Application US/09840707A  
; Patent No. US2002007726A1  
; GENERAL INFORMATION:  
; APPLICANT: Fredexing, Terry M.  
; APPLICANT: Ignatyev, George M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS  
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS  
; FILE REFERENCE: 24881-301C  
; CURRENT APPLICATION NUMBER: US/09/840,707A  
; CURRENT FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: 09/562,979  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/198,210  
; PRIOR FILING DATE: 1999-04-27  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Tumor Necrosis Factor p55 Receptor  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AAA36753/GenBank  
; DATABASE ENTRY DATE: 1995-08-03  
US-09-840-707A-16

Query Match 98.6%; Score 579; DB 9; Length 455;  
Best Local Similarity 99.1%; Pred. No. 1.3e-57;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKQSLDTPATLYAVVENPPLRWKKEFVKRLGLSDHEIDRLQLONGRCCLREAYQY 61  
DB 345 AHKQSLDTPATLYAVVENPPLRWKKEFVKRLGLSDHEIDRLQLONGRCCLREAYQY 404  
QY 62 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
DB 405 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

## RESULT 9

US-09-252-656B-3  
; Sequence 3, Application US/09252656B  
; Patent No. US20020081647A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ruben, Steven M.  
; APPLICANT: Zhang, Jun  
; APPLICANT: Ullrich, Stephen  
; APPLICANT: Zhai, Yifan  
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
; FILE REFERENCE: 1488.065006  
; CURRENT APPLICATION NUMBER: US/09/252,656B  
; CURRENT FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: US 60/075,409  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: US 09/027,287  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: US 09/003,886  
; PRIOR FILING DATE: 1998-01-07  
; PRIOR APPLICATION NUMBER: US 08/822,953

; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/013,923  
; PRIOR FILING DATE: 1996-03-22  
; PRIOR APPLICATION NUMBER: US 60/030,157  
; PRIOR FILING DATE: 1996-10-31  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-252-656B-3

Query Match 98.6%; Score 579; DB 9; Length 455;  
Best Local Similarity 99.1%; Pred. No. 1.3e-57;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKQSLDTPATLYAVVENPPLRWKKEFVKRLGLSDHEIDRLQLONGRCCLREAYQY 61  
DB 345 AHKQSLDTPATLYAVVENPPLRWKKEFVKRLGLSDHEIDRLQLONGRCCLREAYQY 404  
QY 62 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
DB 405 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

## RESULT 10

US-09-899-422-2  
; Sequence 2, Application US/09899422  
; Patent No. US20020090676A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmler, Adolph  
; APPLICANT: Maurer-Pogoy, Ingrid  
; APPLICANT: Stratowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; TITLE OF INVENTION: Them  
; FILE REFERENCE: 98,385-H  
; CURRENT APPLICATION NUMBER: US/09/899,422  
; CURRENT FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: 09/525,998  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-899-422-2

Query Match 98.6%; Score 579; DB 9; Length 455;  
Best Local Similarity 99.1%; Pred. No. 1.3e-57;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKQSLDTPATLYAVVENPPLRWKKEFVKRLGLSDHEIDRLQLONGRCCLREAYQY 61  
DB 345 AHKQSLDTPATLYAVVENPPLRWKKEFVKRLGLSDHEIDRLQLONGRCCLREAYQY 404  
QY 62 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
DB 405 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

## RESULT 11

US-09-899-422-17

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; Sequence 17, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
; OTHER INFORMATION: LTNF-R2
US-09-899-422-17

Query Match          98.6%; Score 579; DB 9; Length 455;
Best Local Similarity 99.1%; Pred. No. 1.3e-57;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKQSLDTPATLYAVVNPPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQSML 61
DB 345 AHKQSLDTPATLYAVVNPPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQSML 404

QY 62 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEALCGPAALPPAPSLR 112
DB 405 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEALCGPAALPPAPSLR 455

RESULT 12
US-09-935-727-5
; Sequence 5, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-727-5

Query Match          98.6%; Score 579; DB 9; Length 455;
Best Local Similarity 99.1%; Pred. No. 1.3e-57;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKQSLDTPATLYAVVNPPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQSML 61
DB 345 AHKQSLDTPATLYAVVNPPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQSML 404

QY 62 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEALCGPAALPPAPSLR 112
DB 405 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEALCGPAALPPAPSLR 455

RESULT 13
US-09-898-234-2
; Sequence 2, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-234-2

Query Match          98.6%; Score 579; DB 9; Length 455;
Best Local Similarity 99.1%; Pred. No. 1.3e-57;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKQSLDTPATLYAVVNPPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQSML 61
DB 345 AHKQSLDTPATLYAVVNPPLRWKEFVKRLGLSDHEIDRLQNGRCLEAQSML 404

QY 62 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEALCGPAALPPAPSLR 112
DB 405 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEALCGPAALPPAPSLR 455
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## RESULT 14

US-09-898-234-17  
; Sequence 17, Application US/09898234  
; Patent No. US20020155112A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmler, Adolph  
; APPLICANT: Maurer-Poggy, Ingrid  
; APPLICANT: Stracowsa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; TITLE REFERENCE: Them  
; FILE REFERENCE: 98,385-1  
; CURRENT APPLICATION NUMBER: US/09/898,234  
; CURRENT FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 09/525,998  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in  
; OTHER INFORMATION: lTNF-R2  
US-09-898-234-17

Query Match 98.6%; Score 579; DB 9; Length 455;

Best Local Similarity 99.1%; Pred. No. 1.3e-57;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGSLDHEIDRLBLONGRCCLREAQYSML 61  
DB 345 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGSLDHEIDRLBLONGRCCLREAQYSML 404  
QY 62 ATWRRRTPRREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPAPSLLR 112  
DB 405 ATWRRRTPRREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPAPSLLR 455

## RESULT 15

US-09-756-854-5  
; Sequence 5, Application US/09756854  
; Patent No. US20020164684A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; Yu, Guo-Liang  
; Fan, Ping  
; Gentz, Reiner  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/756,854

FILING DATE: 10-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/095,094  
; FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
; NAME: Hoover, Kenley K.  
; REGISTRATION NUMBER: 40,302  
; REFERENCE/DOCKET NUMBER: PF375  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-756-854-5

Query Match 98.6%; Score 579; DB 9; Length 455;

Best Local Similarity 99.1%; Pred. No. 1.3e-57;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGSLDHEIDRLBLONGRCCLREAQYSML 61  
DB 345 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGSLDHEIDRLBLONGRCCLREAQYSML 404  
QY 62 ATWRRRTPRREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPAPSLLR 112  
DB 405 ATWRRRTPRREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPAPSLLR 455

Search completed: June 1, 2004, 14:50:03

Job time : 36.2156 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 14:37:07 ; Search time 11.7365 Seconds  
(without alignments)  
917.942 Million cell updates/sec

Title: US-09-854-906-1

Perfect score: 587

Sequence: 1 MAHKPSLTDPTATLYAVV.....DIEEALCGPAALPPAPSLLR 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	579	98.6	455	1 QGHUT1	tumor necrosis fac
2	459.5	78.3	461	2 JCA302	tumor necrosis fac
3	384	65.4	461	1 QORUT1	tumor necrosis fac
4	347.5	59.2	454	1 QOMST1	tumor necrosis fac
5	88.5	15.1	671	2 T09479	serine/threonine p
6	87	14.8	656	2 I49299	receptor interacti
7	83	14.1	1848	2 S37771	ankyrin, erythrocy
8	83	14.1	1862	2 I49502	ankyrin - mouse
9	82	14.0	163	2 B72550	probable methylmal
10	77.5	13.2	591	2 T41531	activator of Hsp70
11	77.5	13.2	591	2 T51996	hypothetical prote
12	77.5	13.2	1765	2 T42714	ankyrin 3, splice
13	77.5	13.2	1940	2 T42715	ankyrin 3, splice
14	77.5	13.2	1943	2 T42713	ankyrin 3, splice
15	77.5	13.2	1961	2 T42716	ankyrin 3, splice
16	77.5	13.2	4377	2 A55575	ankyrin 3, long sp
17	77	13.1	316	2 D83192	acetyl-coenzyme A
18	77	13.1	1856	2 B35049	ankyrin 1, erythro
19	77	13.1	1880	2 A35049	ankyrin 1, erythro
20	77	13.1	1881	1 SJHUK	ankyrin 1, erythro
21	76.5	13.0	388	2 E95177	aminotransferase,
22	76	12.9	536	2 D83419	probable Arp-bindi
23	73.5	12.5	580	2 G82693	glutamyl-tRNA sy
24	72.5	12.4	138	2 S37773	ankyrin, erythrocy
25	72.5	12.4	295	2 A86745	conserved hypothet
26	72.5	12.4	388	2 G98043	aminotransferase (
27	72	12.3	1882	1 GNVVTR	genome polyprotein
28	71.5	12.2	156	2 D39109	genome polyprotein
29	71.5	12.2	208	2 A56912	FADD protein - hum

30	71.5	12.2	426	2 I48379	gene hb protein -
31	71.5	12.2	902	2 A55543	cmaA protein - Pse
32	71.5	12.2	3924	2 S37431	ankyrin 2, neurona
33	71	12.1	812	2 A83379	glycogen phosphory
34	70.5	12.0	402	2 E71279	hypothetical prote
35	70.5	12.0	412	2 E88736	protein F33B4.6a [
36	70.5	12.0	529	2 F84106	hypothetical prote
37	70.5	12.0	672	2 T32557	hypothetical prote
38	70.5	12.0	1083	2 S54293	regulator protein
39	70.5	12.0	1805	2 A34736	nestin - rat
40	70	11.9	533	2 G75348	conserved hypothet
41	70	11.9	643	2 E83142	probable transcrip
42	69.5	11.8	323	2 AD2753	lipoteic Acid Synthe
43	69.5	11.8	323	2 B97534	lipoteic acid synthe
44	69.5	11.8	395	2 F90012	hypothetical prote
45	69.5	11.8	446	2 AD3460	UDP-N-acetylglucos

#### ALIGNMENTS

#### RESULT 1

##### QGHUT1

tumor necrosis factor receptor 1 precursor [validated] - human  
N;Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1  
N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1992 #sequence revision 10-Jun-1992 #text change 08-Dec-2000  
C;Accession: A38208; A34899; A34900; A36555; C36555; S12057; J07058; A60231; A38  
R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.  
Genomics 13, 219-224, 1992  
A;Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to ch  
A;Reference number: A38208; MUID:92250049; PMID:131517  
A;Accession: A38208  
A;Molecule type: DNA  
A;Residues: 1-455 <FUC>  
A;Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PID:g  
R;Loetscher, H.; Pan, Y.C.E.; Laht, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau  
Cell 61, 351-359, 1990  
A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor rece  
A;Reference number: A34899; MUID:90235284; PMID:2158862  
A;Accession: A34899  
A;Molecule type: mRNA  
A;Residues: 1-455 <LOE>  
A;Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754  
A;Experimental source: placenta  
A;Note: part of this sequence, including the amino end of the mature protein, confirmed  
R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.  
Cell 61, 361-370, 1990  
A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.  
A;Reference number: A34900; MUID:30235285; PMID:2158863  
A;Accession: A34900  
A;Molecule type: mRNA  
A;Residues: 1-455 <SCH>  
A;Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745  
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;  
DNA Cell Biol. 9, 705-715, 1990  
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto  
A;Reference number: A36555; MUID:91090841; PMID:1702293  
A;Accession: A36555  
A;Molecule type: mRNA  
A;Residues: 1-455 <CHIM>  
A;Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756  
A;Accession: C36555  
A;Molecule type: protein  
A;Residues: 30-38;41-53,'X','55-79,'XX','82-94,'NK','XX',100-104;107-128;162-167,'X',169-2  
A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble  
R;Gray, P.W.; Barrett, K.; Chantray, D.; Turner, M.; Feldmann, M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990  
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re  
A;Reference number: A38281; MUID:91017509; PMID:2170974  
A;Accession: A38281  
A;Molecule type: mRNA

A;Residues: 1-455 <GRA>  
A;Cross-references: GB:M37764  
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372  
R;Noplar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Wang, R.; Aderka, D.; Holtmann  
EMBO J. 9, 3269-3278, 1990  
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type  
I form of the receptor.  
A;Reference number: S12057; PMID:91006021; PMID:1698610  
A;Accession: S12057  
A;Molecule type: mRNA  
A;Residues: 1-455 <NOP>  
A;Cross-references: EMBL:X55313; NID:g37223; PIDN:CRA39021.1; PID:g37224  
A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, was  
R;Kemper, O.; Wallach, D.  
Gene 134, 209-216, 1993  
A;Title: Cloning and partial characterization of the promoter for the human p55 tumor necrosis  
factor receptor.  
A;Reference number: JTO758; PMID:94085779; PMID:8262379  
A;Accession: JTO758  
A;Molecule type: DNA  
A;Residues: 1-13 <KEM>  
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayner, J.M.  
Eur. J. Immunol. 20, 1167-1174, 1990  
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence  
determination, and characterization of an inhibitor (soluble tumor necrosis factor  
inhibitor).  
A;Reference number: A60231; PMID:90292116; PMID:2113477  
A;Accession: A60231  
A;Molecule type: protein  
A;Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>  
R;Gatanaga, T.; Huang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le  
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor  
inhibitor).  
A;Reference number: A38258; PMID:91062364; PMID:2174164  
A;Accession: A38258  
A;Molecule type: protein  
A;Residues: 41-60 <GAR>  
A;Experimental source: cancer patient serum  
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.  
Eur. J. Haematol. 42, 270-275, 1989  
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from  
human urine.  
A;Reference number: A60594; PMID:89171156; PMID:2924890  
A;Accession: A60594  
A;Molecule type: protein  
A;Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>  
A;Experimental source: renal failure patient urine  
R;Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
for two distinct binding sites.  
A;Reference number: A35010; PMID:90110215; PMID:2153136  
A;Accession: A35010  
A;Molecule type: protein  
A;Residues: 41-45 <ENG>  
A;Experimental source: normal urine  
R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
Biochem. Biotechnol. 58, 2266-2268, 1994  
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from  
human urine.  
A;Reference number: JC2404; PMID:95128033; PMID:7765720  
A;Accession: JC2404  
A;Molecule type: protein  
A;Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>  
A;Experimental source: urine  
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
TNF-beta (lymphotoxin).  
A;Gene: GDB:TNFR1  
A;Cross-references: GDB:125913; OMIM:191190  
A;Map position: 12p13.2-12p13.2  
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat  
homology  
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>  
F;30-211/Domain: extracellular #status predicted <EXT>  
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
predicted <EXT>  
F;44-82/Domain: NGF receptor repeat homology <NGI>

F;84-126/Domain: NGF receptor repeat homology <NG2>  
F;127-167/Domain: NGF receptor repeat homology <NG3>  
F;168-196/Domain: NGF receptor repeat homology <NG4>  
F;212-234/Domain: transmembrane #status predicted <MEM>  
F;235-455/Domain: intracellular #status predicted <INT>  
F;54,145,151/Binding site: carbohydrate (Asn) #status predicted  
Query Match 98.6%; Score 579; DB 1; Length 455;  
Best Local Similarity 99.1%; Pred. No. 5.3e-52;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AHKQSLDTPDPAITYAVVENVPLRWKEFVKRLGLSDHEIDRLLELONGRCLEAQAQYSL 61  
DB 345 AHKQSLDTPDPAITYAVVENVPLRWKEFVKRLGLSDHEIDRLLELONGRCLEAQAQYSL 404  
QY 62 ATWRRTPRREATLELLGRVLRDMDLLGCLDEIEALCGPAALPPAPSLR 112  
DB 405 ATWRRTPRREATLELLGRVLRDMDLLGCLDEIEALCGPAALPPAPSLR 455  
RESULT 2  
JC4302  
tumor necrosis factor receptor p55 precursor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Jul-1999  
C;Accession: JC4302; PC4093  
R;Suter, B.; Pauli, U.  
Gene 163, 263-266, 1995  
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.  
A;Reference number: JC4302; PMID:96011645; PMID:7590278  
A;Accession: JC4302  
A;Molecule type: mRNA  
A;Residues: 1-461 <SUT>  
A;Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753  
A;Accession: PC4093  
A;Molecule type: protein  
A;Residues: 1-7 <SU2>  
A;Experimental source: kidney cell line 15  
C;Genetics:  
A;Gene: tnfr  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>  
F;44-194/Domain: extracellular cyatene rich #status predicted <EXT>  
F;44-82/Domain: NGF receptor repeat homology <NGI>  
F;84-126/Domain: NGF receptor repeat homology <NGF>  
F;211-231/Domain: transmembrane #status predicted <TMM>  
F;361-447/Domain: signal transduction #status predicted <SIT>  
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 78.3%; Score 459.5; DB 2; Length 461;  
Best Local Similarity 82.1%; Pred. No. 1.2e-39;  
Matches 92; Conservative 4; Mismatches 15; Indels 1; Gaps 1;  
QY 2 AHK-QPSLDTPDPAITYAVVENVPLRWKEFVKRLGLSDHEIDRLLELONGRCLEAQAQYSL 60  
DB 350 AHSAPQLADADPAITYAVVDGVPPTWKKEFVKRLGLSEIELELONGRCLEAQAQYSL 409  
QY 61 LATWRRTPRREATLELLGRVLRDMDLLGCLDEIEALCGPAALPPAPSLR 112  
DB 410 LAEWRRTPRREATLELLGLSLVLRDMDLLGCLDEIEALRGPAALPAPHLR 461  
RESULT 3  
GQRT1  
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1992 #sequence\_revision 07-Oct-1994 #text\_change 22-Jun-1999  
C;Accession: B36555  
R;Hammler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;  
DNA Cell Biol. 9, 705-715, 1990

R;Bebo, B.F.  
Immunogenetics 39, 450-451, 1994  
A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell  
A;Reference number: I54532; MUID:94245292; PMID:8188324  
A;Accession: I54532  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-454 <RES>  
A;Cross-references: GB:I26349; NID:g430732; PIDN:AAA59361.1; PID:g430733  
R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.  
Mol. Immunol. 30, 155-176, 1993  
A;Title: Genomic organization and promoter function of the murine tumor necrosis factor  
A;Reference number: I57826; MUID:93156721; PMID:8381516  
A;Accession: I57826  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-393, G', 395-454 <RE2>  
A;Cross-references: GB:I76656; NID:g202100; PIDN:AAA4045.1; PID:g202102  
C;Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca  
C;Genetics:  
A;Gene: TNFR-2  
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
F;30-312/Domain: extracellular #status predicted <EXT>  
F;44-82/Domain: NGF receptor repeat homology <NG1>  
F;84-126/Domain: NGF receptor repeat homology <NG2>  
F;127-167/Domain: NGF receptor repeat homology <NG3>  
F;168-204/Domain: NGF receptor repeat homology <NG4>  
F;213-235/Domain: transmembrane #status predicted <MEM>  
F;236-454/Domain: intracellular #status predicted <INT>  
F;454,151,202/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 59.2%; Score 347.5; DB 1; Length 454;  
Best Local Similarity 68.3%; Pred. No. 4.4e-28;  
Matches 69; Conservative 11; Mismatches 20; Indels 1; Gaps 1;

QY 2 AHKPSGLDDDPATLYAVVENVPPLRWKEFVKRLGSLSDHEIDRLQLNGRCLEAQYSML 61  
346 AH-PORPDNADILYAVVDGPPARWKEFMFGSLSHSEIERLEWQNGRCLEAQYSML 404  
DB  
QY 62 ATWRRRTPREATLELGRVLRMDMLLGCEIDIEALCGPA 102  
405 EAWRRRTPREHTLEWVGLVSKNNLAGCLENILEALRNPA 445  
DB

RESULT 5  
T09479  
serine/threonine protein kinase (EC 2.7.1.1-) RIP - human  
C;Species: Homo sapiens (man)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 17-Nov-2000  
C;Accession: T09479; I38992  
R;Huang, J.; Hsu, H.; Baichwal, V.R.; Goeddel, D.V.  
submitted to the EMBL Data Library, August 1998  
A;Reference number: Z16685  
A;Accession: T09479  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-671 <HUA>  
A;Cross-references: EMBL:U50062; NID:g3426026; PID:g3426027  
R;Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.  
Cell 81, 513-523, 1995  
A;Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1 (C  
A;Reference number: A56913; MUID:95277838; PMID:7538908  
A;Accession: I38992  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 300-513, 'S', 515-671 <RES>  
A;Cross-references: EMBL:U25994; NID:g829616; PIDN:AAC50137.1; PID:g829617  
C;Genetics:  
A;Gene: RIP

**C;Keywords:** ATP binding; phosphotransferase

```
Query Match      15.1%; Score 88.5; DB 2; Length 671;
Best Local Similarity 27.0%; Pred. No. 0.39;
Matches         27; Conservative 18; Mismatches 36; Indels 19; Gaps 4

QY    11 DPBPATLYAV-----ENVPLR-----WKEFVKRLGSLSDHIDRLLELONGER-CUR 54
       :||| :          :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db     566 EPPAAKYQAIFDNTTSLTDKHLDPITRENGLGHKNWCARKLGFQSQIDEIHDHYERDGILK 625

QY    55 EAQYSMLATWRRTPRREATLELLGRVIRD---MDLLIGCL 91
       :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db     626 EKYYQLQKWNRREGIKGTATGYKLGAQHQCSTRIDLSSLL 665
```

## RESULT 6

I49299  
receptor interacting protein RIP - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 05-Nov-1999  
C:Accession: I49299  
R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.  
Cell 81, 513-523, 1995  
A:Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1 (CD  
A:Reference number: A56913; MUID:95277839; PMID:7538908  
A:Accession: I49299  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-656 <RES>  
A:Cross-references: EMBL:U25995; NID:9829618; PIDN:AAS60487.1; PID:g829619  
C:Genetics:  
A:Gene: RIP  
C:Superfamily: protein kinase homology  
F:15-293/Domain: protein kinase homology <KIN>

```

Query Match      14.8%; Score 87; DB 2; Length 656;
Best Local Similarity 30.9%; Pred. No. 0.54;
Matches 25; Conservative 15; Mismatches 31; Indels 10; Gaps 3;

QY 21 ENVPELR-----WKSEFKVLGSDHIDKLELQNGR-CLREAQYSMLATWRRTPPRA 73
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 570 EHLNFRLENLGRWQKNCARLKGFTESQIDRIDHYERDGLKEKYQMLQKLMREGTKGA 629
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 74 TLELLGRVLRD---MDLLGCL 91
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 630 TVGKLAQALHCCCRIDLLNHL 650
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

## RESULT 7

ankyrin, erythrocyte - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 27-May-1994 #sequence\_revision 03-Aug-1995 #text\_change 13-Aug-1999  
 C:Accession: S37771  
 R:Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.  
 J. Biol. Chem. 268, 9533-9540, 1993  
 A:Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found am  
 A:Reference number: S37771; MUID:93252825; PMID:8486643  
 A:Accession: S37771  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1848 <BR>  
 A:Cross-references: EMBL:X59063; NID:g311816; PIDN:CAN48801.1; PID:g311817  
 C:Superfamily: ankyrin; ankyrin repeat homology  
 C:Keywords: alternative splicing  
 F:48-80/Domain: ankyrin repeat homology <AN01>  
 F:81-113/Domain: ankyrin repeat homology <AN02>  
 F:114-146/Domain: ankyrin repeat homology <AN03>  
 F:147-175/Domain: ankyrin repeat homology <AN04>  
 F:176-208/Domain: ankyrin repeat homology <AN05>  
 F:209-241/Domain: ankyrin repeat homology <AN06>  
 F:242-274/Domain: ankyrin repeat homology <AN07>  
 F:275-307/Domain: ankyrin repeat homology <AN08>

F:308-340/Domain:	ankyrrin	repeat	homology	<AN09>
F:341-373/Domain:	ankyrrin	repeat	homology	<AN10>
F:374-406/Domain:	ankyrrin	repeat	homology	<AN11>
F:407-439/Domain:	ankyrrin	repeat	homology	<AN12>
F:440-472/Domain:	ankyrrin	repeat	homology	<AN13>
F:473-505/Domain:	ankyrrin	repeat	homology	<AN14>
F:506-538/Domain:	ankyrrin	repeat	homology	<AN15>
F:539-571/Domain:	ankyrrin	repeat	homology	<AN16>
F:572-604/Domain:	ankyrrin	repeat	homology	<AN17>
F:605-637/Domain:	ankyrrin	repeat	homology	<AN18>
F:638-670/Domain:	ankyrrin	repeat	homology	<AN19>
F:671-703/Domain:	ankyrrin	repeat	homology	<AN20>
F:704-736/Domain:	ankyrrin	repeat	homology	<AN21>
F:737-769/Domain:	ankyrrin	repeat	homology	<AN22>
F:770-802/Domain:	ankyrrin	repeat	homology	<AN23>

Query Match	14.1%	Score 83;	DB 2;	Length 1848;
Best Local Similarity	22.6%	Pred. No. 4.6;		
Matches 31;	Conservative 20;	Mismatches 48	Indels	

Qy	9	DTDDPATLYAVENVPLRWKEFVKBLGLSDHEIDRLLELQNGRCLEARYSMLATWRRRT	68
Dd	1411	DTDVRMBMAVIREHLGLSWAELRELQFSVEDINRIVENPNLSLDQSTALLTLMWDR-	1469
Qy	69	PREATLELLGRVLRMD---LLGCLUE-----DI	94
Dd	1470	EGENAKMENLYALRNIDRSEIWNMLEVSGRQSNLKPKERRHGDREYSLSPSQVNGYSSL	1529
Qy	95	EEALCGPAALP----PAP	108
Dd	1530	QDELLSPASLOVALPSP	1546

## RESULT 8

I49502  
anMyrin - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
C;Accession: I49502  
R;White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.  
Mamm. Genome 3, 281-285, 1992  
A;Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory do  
A;Reference number: I49502; MUID:92345717; PMID:1386265  
A;Accession: I49502  
A;Status: preliminary; translated from GB/EMBL/DBDJB  
A;Molecule type: mRNA  
A;Residues: 1-1862 <RES>  
A;Cross-references: GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:g191940  
C;Genetics:



Query Match	13.2%;	Score 77.5;	DB 2;	Length 1765;
Best Local Similarity	28.6%;	Pred. No. 16;		
Matches 24;	Conservative 15;	Mismatches 40;	Indels 5;	Gaps 2;

```

QY      18 AVTVNVPPIRWKFEVKVLGLSDHEIDLELQNGRCLEEAQYSMLATWRRTPRREATLEL 77
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db     1493 AIVADHUGLSWTEARELNFSVDEINIRVENPENSLLISQSFMILLKKVVTR-DGKNATTDA 1541
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||:
QY      78 LGRVLRDMDLGLCLIEDIEEALCGP 101
       ||||::||::||::||::||::||::||::||::||::||::||::||::||:
Db     1542 LTSVLTKINRI---DIVTLLEGP 1561
       ||||::||::||::||::||::||::||::||::||::||::||::||::||:

RESULT 13
T42715
ankyrin 3, splice form 3 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C/Accession: T42715
R/Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, I.
J. Cell Biol. 130, 313-330, 1995
A>Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A/Reference number: Z22337; MUID:95340633; PMID:7615634
A/Accession: T42715
A>Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-1940 <PET>
A/Cross-references: EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604.1
A/Experimental source: strain C57BL/6J; kidney
C/Genetics:
A/Gene: Ank3
A/Map position: 10
A/Introns: 834/1
C/Superfamily: ankyrin; ankyrin repeat homology
C/Keywords: alternative splicing

```

Query Match	13.2%;	Score 77.5;	DB 2;	Length 1940;
Best Local Similarity	28.6%;	Pred. No. 18;		
Matches 24;	Conservative	15;	Mismatches 40;	Indels 5;
			Gaps 2;	

QY	18	AVVENVPURKGFVKRLGLSDHIEDRLUQLONGCLREAOYSMLATWRRRTTPREATJEL	77
DB	1462	AIYADHLGLSWTELARELNFSDVEINQVVENPSLISQSFMLLKKWYTR-DGKNATTD	1520

```

QY      78  LGRVLRMDLLGCLEDEIEEALCGP 101
      |  | | | : : | | | | |
Db      1521 LTSVLTKNIRI----DIVTLLEGP 1540

```

RESULT 14  
T42713  
ankyrin 3, splice form 1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 04-Mar-2000  
C:Accession: T42713  
J:Peterson, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.  
J. Cell Biol. 130, 313-330, 1995  
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene  
the repeat domain.  
A:Reference number: Z22237; MUID:95340633; PMID:7615634  
A:Accession: T42713  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1943 <P>  
A:Cross-references: EMBL:L40632; NID:G710548; PID:G710550; PIDN:AAB01606.1  
A:Experimental source: strain C57BL/6J; kidney  
C:Genetics:  
A:Gene: Ank3  
A:Map position: 10  
A:Introns: 855/1  
C:Function:  
A:Description: supposed to play an important role in the polarized distribution of many  
A>Note: major kidney ankyrin  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing

```

Query Match      13.2%; Score 77.5; DB 2; Length 1943;
Best local Similarity 28.6%; Pred.No.18;
Matches 24; Conservative 15; Mismatches 40; Indels 5; Gaps 2;

QY      18 AVVENPPLRWKFEVKRLGLSDHEIDRLQLNGRCLEAAQYSMLATWRRRTTREATL 77
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db       1465 AIVADHUGLGSWTELARELNFSVEINQIRVENPNSLISQSFMLEKKWVR -DGNATTTDA 1523
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      78 LGRVLRDMDLGLGCLIEDIEALCGP 101
      ||| : : ||| |||
Db       1524 LTSVLTKINEL---DIVTLEGP 1543
      ||| : : ||| |||

RESULT 15
T42716
ankyrin 3, splice form 4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C:Accession: T42716
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo,
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: Z22237; MUID:95340633; PMID:7615634
A:Accession: T42716
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1961 <ET>
A:Cross-references: EMBL:L40632; NID:g710548; PID:g710552; PIDN:AAB01607.1
A:Experimental source: strain C57BL/6J; kidney

```

A:Gene: ANK3  
A:Map position: 10  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing

Query Match	13.2%;	Score 77.5;	DB 2;	Length 1961;
Best Local Similarity	28.6%;	Pred. No. 18;		
Matches 24;	Conservative	15;	Mismatches 40;	Indels 5;
				Gaps 2;

QY	18	AVVENVP	PLRWKEFV	KVRLGSL	SHSHEID	RUELO	NGRC	LRQAQY	SMLATW	RRRTTP	REATU	EL 77
DB	1483	AIYADH	LGSLSWT	ELAREL	NFSVDE	INQV	ENEN	SLTSQ	SFELLK	QWTR	-DGNK	ATDA 154

Qy 78 IGRVIRDMDLGLCLEDIEEALCGP 101  
| | | : : | | |  
db 1542 LTSVLTKNRI----DIVTLLEGP 1561

Search completed: June 1, 2004, 14:47:08  
Job time : 12.7365 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:33:56 ; Search time 8.0479 Seconds  
(without alignments)  
724.643 Million cell updates/sec

Title: US-09-854-906-1

Perfect score: 587

Sequence: 1 MAHKPQLDTPDPTLYAVV.....DIERALCGPAALPPAPSLLR 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	579	98.6	1 TRIA_HUMAN	P19438 homo sapien
2	459.5	78.3	1 TRIA_PIG	P50555 sus scrofa
3	421	71.7	1 TRIA_BOVIN	O19131 bos taurus
4	384	65.4	1 TRIA_RAT	P22934 rattus norv
5	347.5	59.2	1 TRIA_MOUSE	P25118 mus musculu
6	164.5	28.0	1 TR25_HUMAN	Q93038 h tumor nec
7	97	16.5	1 T10B_MOUSE	Q9qzm4 mus musculu
8	88.5	15.1	1 RIKI_HUMAN	Q13546 homo sapien
9	87	14.8	1 RIKI_MOUSE	Q60855 mus musculu
10	83	14.1	1 ANK1_MOUSE	Q02357 mus musculu
11	77.5	13.2	1 STI1_SCHPO	Q9usi5 schizosacch
12	77.5	13.2	1 ANK3_HUMAN	O12955 homo sapien
13	77	13.1	1 ANK1_HUMAN	P16157 homo sapien
14	73.5	12.5	1 T10B_HUMAN	O14763 homo sapien
15	73.5	12.5	1 SYQ_XYLEFA	Q9pdp1 xyellia fas
16	73	12.4	1 Y173_HUMAN	Q14679 homo sapien
17	72.5	12.4	1 YJIE_LACLA	Q9G9Y1 lactococcus
18	72	12.3	1 POL2_TRSVR	P25247 tomato ring
19	71.5	12.2	1 FADD_HUMAN	Q13158 homo sapien
20	71.5	12.2	1 SYQ_XYLEFT	Q87du6 xyellia fas
21	71.5	12.2	1 RHG7_MOUSE	Q9x029 mus musculu
22	71.5	12.2	1 ANK2_HUMAN	Q61484 homo sapien
23	70.5	12.0	1 RHG7_RAT	Q63744 x rho-gtase
24	70.5	12.0	1 NEST_RAT	P21263 rattus norv
25	69.5	11.8	1 LIPA_AGR5	Q8uf91 agrobacteri
26	69.5	11.8	354	Q86ym7 homo sapien
27	69.5	11.8	1 MURA_BRUME	Q8Yf61 bruceella me
28	69.5	11.8	1 RHG7_HUMAN	Q96gb1 homo sapien
29	69	11.8	1 TPH_XENLA	Q92142 xenopus lae
30	69	11.8	1 PMC2_MOUSE	P56960 mus musculu
31	68.5	11.7	1 SPCF_HUMAN	O15020 homo sapien
32	68	11.6	1 TPH1_CHICK	P70080 gallus gall
33	68	11.6	1 ICBA_HUMAN	Q92851 homo sapien

34	67.5	11.5	384	1 BRH2_RAT	O88181 rattus norv
35	67	11.4	885	1 PMC2_HUMAN	Q01780 homo sapien
36	66.5	11.3	189	1 Y135_PASMU	Q9ck03 pasteurella
37	66.5	11.3	366	1 HOM1_MOUSE	Q92y3 mus musculu
38	66.5	11.3	456	1 PYRC_METWA	Q8pvy4 methanosarc
39	66.5	11.3	467	1 YG3H_YEAST	P53285 saccharomyc
40	66.5	11.3	781	1 NANH_VIBCH	P37060 vibrio chol
41	66	11.2	1618	1 NEST_HUMAN	P48681 homo sapien
42	65.5	11.2	205	1 FADD_MOUSE	Q61160 mus musculu
43	65.5	11.2	322	1 LIPA_RHIME	Q92q94 rhizobium m
44	65	11.1	150	1 YAO2_SCHPO	Q10081 rhizosacch
45	65	11.1	554	1 PYRG_CORGL	Q8ng17 corynebacte

## ALIGNMENTS

### RESULT 1

ID	TRIA_HUMAN	STANDARD;	PRT;	455 AA.
AC	P19438;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)			
DE	(TNF-R1) (TNF-RI) (p55) (CD120a) [Contains: Tumor necrosis factor			
DE	binding protein 1 (TNFRI)]			
CN	TNFRSF1A OR TNFR1 OR TNFR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=90235285; PubMed=2158863;			
RA	Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,			
RA	Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;			
RT	"Molecular cloning and expression of a receptor for human tumor			
RT	necrosis factor.";			
RL	Cell 61:361-370(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90235284; PubMed=2158862;			
RA	Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,			
RA	Tabuchi H., Jesslauer W.;			
RT	"Molecular cloning and expression of the human 55 kd tumor necrosis			
RT	factor receptor.";			
RL	Cell 61:351-359(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.			
RX	MEDLINE=91006021; PubMed=1698610;			
RA	Nopnar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,			
RA	Aderka D., Holtmann H., Wallach D.;			
RT	"Soluble forms of tumor necrosis factor receptors (TNF-Ra). The cDNA			
RT	for the type I TNF-R, cloned using amino acid sequence data of its			
RT	soluble form, encodes both the cell surface and a soluble form of the			
RT	receptor.";			
RL	EMBO J. 9:3269-3278(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91090841; PubMed=1702293;			
RA	Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,			
RA	Lantz M., Olson I., Hauptmann R., Stratowa C., Adolf G.R.;			
RT	"Molecular cloning and expression of human and rat tumor necrosis			
RT	factor receptor chain (p60) and its soluble derivative, tumor			
RT	necrosis factor-binding protein.";			
RL	DNA Cell Biol. 9:705-715(1990).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=91017509; PubMed=2170974;			
RA	Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;			



Query Match 98.6%; Score 579; DB 1; Length 455;  
 Best Local Similarity 99.1%; Pred. No. 7.6e-53;  
 Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSQSDTDDPATLYAVVNPPLRWKFEVRLGLSDHEIDRLQNGRCLEAQY5ML 61  
 DB 345 AHKPSQSDTDDPATLYAVVNPPLRWKFEVRLGLSDHEIDRLQNGRCLEAQY5ML 404

QY 62 ATWRRTPREATELLGRVLRDMLGCLDEEALCGPAALPPAPSLR 112  
 DB 405 ATWRRTPREATELLGRVLRDMLGCLDEEALCGPAALPPAPSLR 455

RESULT 2  
 TRIA\_PIG STANDARD; PRT; 461 AA.

AC P50555;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
 DE (TNF-R1) (TNF-R1) (p55).  
 GN TNFRSF1A OR TNFR1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=96011645; PubMed=7590278;  
 RA Suter B., Pauli U.H.;  
 RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.";  
 RL Gene 163:263-266(1995).

CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activated receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis (By similarity).  
 CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to  
 CC homotrimerization. The aggregated death domains provide a novel  
 CC molecular interface that interacts specifically with the death  
 CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
 CC RIP and possibly FADD, are recruited to the complex by their  
 CC association with TRADD. This complex activates at least two  
 CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
 CC Binds BAG4 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -!- SIMILARITY: Contains 1 death domain.

CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CC EMBL: U19994; AAC48499.1; --  
 CC PIR: JC4302; JC4302.  
 CC HSP: P19438; INR.  
 CC InterPro: IPR000488; Death.  
 CC InterPro: IPR001368; TNFR\_c6.  
 CC Pfam: PF00531; death; 1.  
 CC Pfam: PF00020; TNFR\_c6; 3.  
 CC SMART: SM00005; DEATH; 1.  
 CC SMART: SM00208; TNFR; 4.  
 CC PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 CC PROSITE: PS50050; TNFR\_NGFR\_2; 2.

DR PROSITE: PS50017; DEATH DOMAIN; 1.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 21  
 FT CHAIN 22 461  
 FT  
 FT  
 FT DOMAIN 22 210  
 FT TRANSMEM 211 233  
 FT DOMAIN 234 461  
 FT CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 195  
 FT DOMAIN 340 350  
 FT DOMAIN 362 447  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 194  
 FT DISULFID 185 190  
 FT CARBOHYD 54 54  
 FT CARBOHYD 86 86  
 FT CARBOHYD 145 145  
 FT CARBOHYD 151 151  
 SQ SEQUENCE 461 AA; 50696 MW; CD72361BC60C9D43 CRC64;

Query Match 78.1%; Score 459.5; DB 1; Length 461;  
 Best Local Similarity 82.1%; Pred. No. 2.2e-40;  
 Matches 99; Conservative 4; Mismatches 15; Indels 1; Gaps 1;

QY 2 AHK-POSQSDTDDPATLYAVVNPPLRWKFEVRLGLSDHEIDRLQNGRCLEAQY5M 60  
 DB 350 AHKAPQALADADPATLYAVVDGVPTRWKEFVRLGLSEHEIERLELQNGRCLEAQY5M 409

QY 61 LATWRRTPREATELLGRVLRDMLGCLDEEALCGPAALPPAPSLR 112  
 DB 410 LAEWRRTPREATELLGRVLRDMLGCLDEEALCGPAALPPAPSLR 461

RESULT 3  
 TRIA\_BOVIN STANDARD; PRT; 471 AA.

AC O19131;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
 DE (TNF-R1) (TNF-R1) (p55).  
 GN TNFRSF1A OR TNFR1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Aorta;  
 RX MEDLINE=98273505; PubMed=9613449;  
 RA Lee E.-K., Kehrl M.E. Jr., Taylor M.J.;  
 RT "Cloning and sequencing of cDNA encoding bovine tumor necrosis factor (TNF)-receptor I.";  
 RL Vet. Immunol. Immunopathol. 51:379-385(1998).  
 CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activated receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC





RIP and possibly FADD, are recruited to the complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NF-kappa-B signaling. Binds BAG4 (By similarity).

!- SUBCELLULAR LOCATION: Type I membrane protein.

!- SIMILARITY: Contains 4 TNFR-Cys repeats.

!- SIMILARITY: Contains 1 death domain.

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DR EMBL; M60468; AAA39751.1; -

DR EMBL; M59377; AAA0464.1; -

DR EMBL; X59238; CAA41922.1; -

DR EMBL; X57796; CAA40936.1; -

DR EMBL; I26349; AAA59361.1; -

DR EMBL; M76656; AAA40465.1; -

DR EMBL; M88067; AAA40465.1; JOINED.

DR EMBL; M76655; AAA40465.1; JOINED.

DR EMBL; BC004599; AAA04599.1; -

DR EMBL; BC052675; AAHS2675.1; -

DR PIR; A38634; GQMST1.

DR HSSP; P19438; 1EXT.

DR MGD; MGI:1314884; Tnfrsfla.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.

DR GO; GO:0006954; P:defense response; IMP.

DR GO; GO:0006954; P:inflammatory response; IMP.

DR GO; GO:0007515; P:lymph gland development; IMP.

DR InterPro; IPR000488; Death.

DR InterPro; IPR001368; TNFR\_C6.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00020; TNFR\_C6; 4.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.

DR PROSITE; PS00652; TNFR\_NGFR\_2; 3.

DR PROSITE; PS00050; TNFR\_NGFR\_3; 3.

DR PROSITE; PS00017; DEATH DOMAIN; 1.

KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 21

FT CHAIN 22 454

FT DOMAIN 22 212

FT TRANSMEM 213 235

FT DOMAIN 236 454

FT REPEAT 43 82

FT REPEAT 83 125

FT REPEAT 126 166

FT REPEAT 167 196

FT DOMAIN 339 349

FT DOMAIN 356 441

FT DISULFID 44 58

FT DISULFID 59 72

FT DISULFID 62 81

FT DISULFID 84 99

FT DISULFID 102 117

FT DISULFID 105 125

FT DISULFID 127 143

FT DISULFID 146 158

FT DISULFID 149 166

FT DISULFID 168 179

FT DISULFID 182 195

FT DISULFID 185 191

FT CARBOHYD 54 54

FT CARBOHYD 151 151

FT CARBOHYD 202 202

FT CONFLICT 394 394

SQ SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C2B6D9 CRC64;

Query Match 59.2%; Score 347.5; DB 1; Length 454;  
Best Local Similarity 68.3%; Pred. No. 1e-28;  
Matches 69; Conservative 11; Mismatches 20; Indels 1; Gaps 1;

QY 2 AHKPSLDTDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLBLONGRCLEAQSML 61  
DB 346 AH-PORPONADLAIYAVVDGVPFARWKEFMRFMGLSEHIERLEWQNGRCLEAQSML 404  
QY 62 ATWRRTERRRATLELLGRVLRDMDLLGLCDEIEEALCGPA 102  
DB 405 EAWRRTRPRHDTLEVVGLVSKMNLACLENILEALNPA 445

RESULT 6

TR25 HUMAN

ID TR25 HUMAN STANDARD; PRT; 417 AA.

AC Q93038; Q00275; Q00276; Q00277; Q00278; Q00279; Q00280; Q14865;  
AC Q14866; P78507; P78515; Q92983; Q93036; Q93037; Q99722; Q99830;  
AC Q99831; Q9BY86; Q9UM60; Q9UM61; Q9UM65;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 25 precursor  
DE (WSL-1 protein) (Apoptosis-mediating receptor DR3) (Apoptosis-  
DE mediating receptor TRAMP) (Death domain receptor 3) (WSL protein)  
DE (Apoptosis inducing receptor AIR) (Apo-3) (Lymphocyte associated  
DE receptor of death) (LARD).  
GN TNFRSF25 OR TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.  
RC TISSUE=Lymphoid;  
RX MEDLINE=97088617; PubMed=8934525;  
RA Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,  
RA Grinham C.J., Brown R., Farrow S.N.;  
RT "A death-domain-containing receptor that mediates apoptosis.";  
RL Nature 384:372-375(1996).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Umbilical vein endothelial cells;  
RX MEDLINE=97081063; PubMed=8875942;  
RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,  
RA Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;  
RT "Signal transduction by DR3, a death domain-containing receptor  
RT related to TNFR-1 and CD95.";  
RL Science 274:990-992(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Heart;  
RX MEDLINE=97148200; PubMed=8994832;  
RA Masters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,  
RA Goddard A.D., Bauer K.D., Ashkenazi A.;  
RT "Apo-3, a new member of the tumor necrosis factor receptor family,  
RT contains a death domain and activates apoptosis and NF-kappa-B.";  
RL Curr. Biol. 6:1669-1676(1996).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).  
RX MEDLINE=97272273; PubMed=9114039;  
RA Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,  
RA McMichael A.J., Bell J.I.;  
RT "LARD: a new lymphoid-specific death domain containing receptor  
RT regulated by alternative pre-mRNA splicing.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).  
RX MEDLINE=98113360; PubMed=9446802;



RA Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,  
 RA Salles G.;  
 RT "A new death receptor 3 isoform: expression in human lymphoid cell  
 RL lines and non-Hodgkin's lymphomas.";  
 RL Biochem. Biophys. Res. Commun. 242:376-379 (1998).  
 [7]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,  
 RA Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 [8]  
 RP SEQUENCE OF 4-417 FROM N.A.  
 RC TISSUE=Brain, and Fetal lung;  
 RX MEDLINE=97205335; PubMed=9052839;  
 RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,  
 RA Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,  
 RA Browning J.L., Macdonald H.R., Tschoep J.;  
 RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology  
 RT to tumor necrosis factor receptor 1 and Fas (Apo-1/CD95).";  
 RL Immunity 6:79-88 (1997).  
 [9]  
 RP SEQUENCE OF 7-417 FROM N.A.  
 RC TISSUE=Brain;  
 RA Chaudhary P.M., Hood L.E.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 [10]  
 RP INTERACTION WITH BAG4.  
 RX MEDLINE=99115917; PubMed=9915703;  
 RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;  
 RT "Prevention of constitutive TNF receptor 1 signaling by silencer of  
 RT death domains";  
 RL Science 283:543-546 (1999).  
 CC -!- FUNCTION: Receptor for TNFSF12/APO3L/TWEAK. Interacts directly  
 CC with the adaptor TRADD. Mediates activation of NF-kappa-B and  
 CC induces apoptosis. May play a role in regulating lymphocyte  
 CC homeostasis.  
 CC -!- SUBUNIT: Homodimer. Interacts strongly via the death domains with  
 CC TNFSF1 and TRADD to activate at least two distinct signaling  
 CC cascades, apoptosis and NF-kappa-B signaling. Interacts with BAG4.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9  
 CC and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)  
 CC (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=12;  
 CC Name=1; Synonyms=WSL-1, LARD-1A;  
 CC IsoId=Q93038-1; Sequence=Displayed;  
 CC Name=2; Synonyms=LARD-1B;  
 CC IsoId=Q93038-2; Sequence=VSP\_006504;  
 CC Name=3; Synonyms=WSL-S1, LARD-3;  
 CC IsoId=Q93038-3; Sequence=VSP\_006497, VSP\_006498;  
 CC Name=4; Synonyms=WSL-S2, LARD-2;  
 CC IsoId=Q93038-4; Sequence=VSP\_006501, VSP\_006502;  
 CC Name=5; Synonyms=LARD-4, LARD-11;  
 CC IsoId=Q93038-5; Sequence=VSP\_006495;  
 CC Name=6; Synonyms=LARD-5;  
 CC IsoId=Q93038-6; Sequence=VSP\_006491, VSP\_006495;  
 CC Name=7; Synonyms=LARD-6;  
 CC IsoId=Q93038-7; Sequence=VSP\_006491, VSP\_006493, VSP\_006494;  
 CC Name=8; Synonyms=LARD-7;  
 CC IsoId=Q93038-8; Sequence=VSP\_006492;  
 CC Name=9; Synonyms=LARD-8;  
 CC IsoId=Q93038-9; Sequence=VSP\_006491;  
 CC Name=10; Synonyms=LARD-9;  
 CC IsoId=Q93038-10; Sequence=VSP\_006503;  
 CC Name=11; Synonyms=Beta;  
 CC IsoId=Q93038-11; Sequence=VSP\_006496;  
 CC Name=12; Synonyms=Beta soluble;  
 CC IsoId=Q93038-12; Sequence=VSP\_006499, VSP\_006500;  
 CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND  
 CC LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,  
 CC COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.  
 CC -!- PTM: Glycosylated (Probable).  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC -!- SIMILARITY: Contains 1 death domain.  
 CC -!- CAUTION: Ref 5 reports for isoform 4 at position 208 a serine  
 CC residue instead of arginine.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; Y09392; CAA70561.1; -  
 CC EMBL; Y09392; CAA70559.1; -  
 CC EMBL; Y09392; CAA70560.1; -  
 CC EMBL; U72763; AAC50819.1; -  
 CC EMBL; U83599; AAB41434.1; -  
 CC EMBL; U83600; AAB41435.1; -  
 CC EMBL; U78029; AAB40918.1; -  
 CC EMBL; U74611; AAB39714.1; -  
 CC EMBL; U94501; AAC51306.1; -  
 CC EMBL; U94504; AAC51309.1; -  
 CC EMBL; U94502; AAC51307.1; -  
 CC EMBL; U94503; AAC51308.1; -  
 CC EMBL; U94505; AAC51310.1; -  
 CC EMBL; U94506; AAC51311.1; -  
 CC EMBL; U94507; AAC51312.1; -  
 CC EMBL; U94508; AAC51313.1; -  
 CC EMBL; U94509; AAC51314.1; -  
 CC EMBL; U94510; AAC51315.1; -  
 CC EMBL; U94512; AAC51316.1; -  
 CC EMBL; U83598; AAB41433.1; -  
 CC EMBL; AF026070; AAC39556.1; -  
 CC EMBL; AF026071; AAB82288.1; -  
 CC EMBL; AB051850; BAB40662.1; -  
 CC EMBL; AB051851; BAB40663.1; -  
 CC EMBL; U75380; AAC51192.1; -  
 CC EMBL; U75381; AAC51193.1; -  
 CC EMBL; U83597; AAB41432.1; -  
 CC Genew; HGNC:11910; TNFRSF25.  
 CC MIM; 603366; -  
 CC GO; GO:0005829; C:cytosol; NAS.  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0016329; F:apoptosis regulator activity; NAS.  
 CC GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.  
 CC GO; GO:0004872; F:receptor activity; NAS.  
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . ; TAS.  
 CC GO; GO:0008624; P:induction of apoptosis by extracellular sig. . ; TAS.  
 CC InterPro; IPR00488; Death.  
 CC InterPro; IPR001368; TNFR\_c6.  
 CC Pfam; PF00531; death; 1  
 CC Pfam; PF00202; TNFR\_c6; 2.  
 CC PROSITE; PS00852; TNFR\_NGFR\_1; 2.  
 CC PROSITE; PS00500; TNFR\_NGFR\_2; 1.  
 CC PROSITE; PS00107; DEATH\_DOMAIN; 1.  
 CC Receptor; Apoptosis; Transmembrane; Alternative splicing; Signal;  
 CC Repeat; Polymorphism.  
 CC SIGNAL 1 24  
 CC CHAIN 25 417  
 CC -----  
 CC DOMAIN 25 199  
 CC TRANSMEM 200 220  
 CC DOMAIN 221 417  
 CC REPEAT 34 71  
 CC REPEAT 72 115  
 CC REPEAT 116 163  
 CC REPEAT 164 192  
 CC DOMAIN 332 413  
 CC DISULFID 35 47  
 CC -----  
 CC FT SIGNAL 1 24  
 CC FT CHAIN 25 417  
 CC -----  
 CC FT DOMAIN 25 199  
 CC FT TRANSMEM 200 220  
 CC FT DOMAIN 221 417  
 CC FT REPEAT 34 71  
 CC FT REPEAT 72 115  
 CC FT REPEAT 116 163  
 CC FT REPEAT 164 192  
 CC FT DOMAIN 332 413  
 CC FT DISULFID 35 47  
 CC -----

Query Match

28.0%;

Score 164.5; DB 1; Length 417;

Best Local Similarity

38.8%;

Pred. No. 1.1e-09;

Matches 40; Conservative 16; Mismatches 32; Indels 15; Gaps 3;



RP SEQUENCE FROM N.A.  
 RA Sycamore N.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 300-671 FROM N.A.  
 RC TISSUE=Leukemic T-cell;  
 RX MEDLINE=95277838; PubMed=7538908;  
 RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;  
 RT "RIP: a novel protein containing a death domain that interacts with  
 RT Fas/APO-1 (CD95) in yeast and causes cell death.";  
 RL Cell 81:513-523(1995).  
 RN [5]  
 RP CLEAVAGE BY CASPASE-8, AND MUTAGENESIS OF ASP-324.  
 RX MEDLINE=99452794; PubMed=10521396;  
 RA Lin Y., Devin A., Rodriguez Y., Liu Z.-G.;  
 RT "Cleavage of the death domain kinase RIP by caspase-8 prompts  
 RT TNF-induced apoptosis.";  
 RL Genes Dev. 13:2514-2526(1999).  
 RN [6]  
 RP INTERACTION WITH RIPK3.  
 RX MEDLINE=99287880; PubMed=10358032;  
 RA Sun X., Lee J., Navas T., Baldwin D.T., Stewart T.A., Dixit V.M.;  
 RT "RIP3, a novel apoptosis-inducing kinase.";  
 RL J. Biol. Chem. 274:16871-16875(1999).  
 RN [7]  
 RP INTERACTION WITH BNL1.  
 RX MEDLINE=99340272; PubMed=10409763;  
 RA Izumi K.M., Cahir McFarland E., Ting A.T., Riley E.A., Seed B.,  
 RA Kieff E.D.;  
 RT "The Epstein-Barr virus oncoprotein latent membrane protein 1 engages  
 RT the tumor necrosis factor receptor-associated proteins TRADD and  
 RT receptor-interacting protein (RIP) but does not induce apoptosis or  
 RT require RIP for NF-kappaB activation.";  
 RL Mol. Cell. Biol. 19:5759-5767(1999).  
 RN [8]  
 RP INTERACTION WITH IKK $\beta$ .  
 RX MEDLINE=99128359; PubMed=9927690;  
 RA Li Y., Kang J., Friedman J., Tarassishin L., Ye J., Kovalenko A.,  
 RA Wallach D., Horwitz M.S.;  
 RT "Identification of a cell protein (FIP-3) as a modulator of NF-kappaB  
 RT activity and as a target of an adenovirus inhibitor of tumor necrosis  
 RT factor alpha-induced apoptosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:1042-1047(1999).  
 RN [9]  
 RP INTERACTION WITH EGFR.  
 RX MEDLINE=21153697; PubMed=11116146;  
 RA Habib A.A., Chatterjee S., Park S.-K., Ratan R.R., Lefebvre S.,  
 RA Vartanian T.;  
 RT "The epidermal growth factor receptor engages receptor interacting  
 RT protein and nuclear factor-kappa B (NF-kappa B)-inducing kinase to  
 RT activate NF-kappa B. Identification of a novel receptor-tyrosine  
 RT kinase signalosome.";  
 RL J. Biol. Chem. 276:8865-8874(2001).  
 RN [10]  
 RP INTERACTION WITH UBCE7IP1.  
 RX MEDLINE=21975204; PubMed=11854271;  
 RA Chen D., Li X., Zhai Z., Shu H.-B.;  
 RT "A novel zinc finger protein interacts with receptor-interacting  
 RT protein (RIP) and inhibits tumor necrosis factor (TNF)- and  
 RT IL1-induced NF-kappa B activation.";  
 RL J. Biol. Chem. 277:15985-15991(2002).  
 CC -!- FUNCTION: Promotes apoptosis and activation of NF-kappa-B.  
 CC Required for TNFRSF1A mediated activation of NF-kappa-B.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SUBUNIT: Binds to the death domain of TNFRSF6 and TRADD. Is  
 CC recruited by TRADD to TNFRSF1A in a TNF-dependent process. Binds  
 CC RIPK3, UBCE7IP1, EGFR, IKK $\beta$ , TRAF1, TRAF2 and TRAF3. Interacts  
 CC with BNL1.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- PTM: Proteolytically cleaved by caspase-8 during TNF-induced  
 CC apoptosis. Cleavage abolishes NF-kappa-B activation and enhances  
 CC pro-apoptotic signaling through the TRADD-FADD interaction.  
 CC -!- PTM: Autophosphorylated on serine and threonine residues.

CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
 CC -!- SIMILARITY: Contains 1 death domain.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U50062; AAC32232.1; -;  
 DR EMBL; AL031963; CAD70625.1; -;  
 DR EMBL; U25994; AAC50137.1; -;  
 DR F01; T09479; T09479.  
 DR HSP; P08631; IAD5.  
 DR Genew; HGNC:10019; RIPK1.  
 DR MIM; 603453; -;  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; TAS.  
 DR GO; GO:0006915; P:apoptosis; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PF00069; TYRKINASE.  
 DR ProDom; PDOM00001; Prot\_kinase; 1.  
 DR SMART; SM00005; DEATH; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS0017; DEATH\_DOMAIN; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation; Apoptosis.  
 FT DOMAIN 17 289 PROTEIN KINASE.  
 FT NP\_BIND 23 31 ATP (BY SIMILARITY).  
 FT BINDING 49 49 ATP (BY SIMILARITY).  
 FT ACT\_SITE 138 138 BY SIMILARITY.  
 FT DOMAIN 583 669 DEATH.  
 FT DOMAIN 411 414 POLY-ARG. (BY CASPASE-8).  
 FT SITE 324 325 CLEAVAGE (BY CASPASE-8).  
 FT MUTAGEN 45 45 K->A: ABOLISHES KINASE ACTIVITY.  
 FT MUTAGEN 324 324 D->K: ABOLISHES CLEAVAGE BY CASPASE-8.  
 FT CONFLICT 438 438 V -> A (IN REF. 3).  
 FT CONFLICT 514 514 T -> S (IN REF. 4).  
 SQ SEQUENCE 671 AA; 75958 MW; BADC4E7E70456ABE CRC64;  
 Query Match 15.1%; Score 88.5; DB 1; Length 671;  
 Best Local Similarity 27.0%; Pred. No. 0.16;  
 Matches 27; Conservative 18; Mismatches 36; Indels 19; Gaps 4;  
 QY 11 DDPATLYAVV-----ENVPELR-----WKEFVRLGLSDHIDRLQLNQR-CLR 54  
 Db 566 EEPAAKYQAFDNTTSLTDKHLDPRENLGHWKNCARKLGTQSQIDEIDHYERDGLK 625  
 QY 55 EAQYSMLATWRRRTPRREATLELGRVLRD--MDLLGLCL 91  
 Db 626 EKVYQMLQKWNRGIGKATVTKLAQALHQCSRIDLSSSL 665  
 RESULT 9  
 RI KL MOUSE  
 ID RI KL MOUSE STANDARD; PRT; 656 AA.  
 AC Q60855; Q8CD90;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)  
 DE (Serine/threonine protein kinase RIP) (Cell death protein RIP)  
 DE (Receptor-interacting protein)  
 GN RIPK1 OR RIP OR RINP.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
 RX MEDLINE=95277838; PubMed=7538908;  
 RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;  
 RA "RIP: a novel protein containing a death domain that interacts with  
 RT Fas/APO-1 (CD95) in yeast and causes cell death.";  
 RL Cell 81:513-523 (1995).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nakai I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wysshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh N., Kagawa A.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573 (2002).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain, and Liver;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Dapkin M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaeetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwen P.J., McKernan K.G., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -!- FUNCTION: Promotes apoptosis and activation of NF-kappa-B.  
 CC Required for TNFRSF1A mediated activation of NF-kappa-B.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SUBUNIT: Binds to the death domain of TNFRSF6 and TRADD. Is  
 CC recruited by TRADD to TNFRSF1A in a TNF-dependent process. Binds

CC RIPK3, UBCE7IP1, EGFR, IKKKG, TRAF1, TRAF2 and TRAF3. Interacts  
 CC with BNL1 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- TISSUE SPECIFICITY: Found at low levels in all tissues.  
 CC -!- PTM: Proteolytically cleaved by caspase-8 during TNF-induced  
 CC apoptosis. Cleavage abolishes NF-kappa-B activation and enhances  
 CC pro-apoptotic signaling through the TRADD-FADD interaction (By  
 CC similarity).  
 CC -!- PTM: Autophosphorylated on serine and threonine residues (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
 CC -!- SIMILARITY: Contains 1 death domain.  
 CC  
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 CC  
 CC EMBL; U25995; AAB60487.1; -;  
 CC EMBL; AK030959; BAC27194.1; -;  
 CC EMBL; BC050905; AAHS0905.1; AUT\_INIT.  
 CC EMBL; BC054542; AAHS4542.1; -;  
 CC EMBL; BC058162; AAHS8162.1; -;  
 CC PIR; I49299; I49299.  
 CC HSP; P25445; 1DDF.  
 CC MGI; MGI:108212; Ripk1.  
 CC InterPro; IPR000488; Death.  
 CC InterPro; IPR000719; Prot\_kinase.  
 CC InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 CC InterPro; IPR01245; Tyr\_pkinase.  
 CC Pfam; PF00531; death; 1.  
 CC Pfam; PF00069; pkinase; 1.  
 CC PRINTS; PR00109; TYRKINASE.  
 CC ProDom; PD000001; Prot\_kinase; 1.  
 CC SMART; SM00005; DEATH; 1.  
 CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE; PS00017; DEATH\_DOMAIN; 1.  
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 KW Apoptosis.  
 FT DOMAIN 17 290 PROTEIN\_KINASE.  
 FT NP\_BIND 23 31 ATP (BY SIMILARITY).  
 FT BINDING 46 46 ATP (BY SIMILARITY).  
 FT ACT\_SITE 138 138 BY SIMILARITY.  
 FT DOMAIN 568 654 DEATH.  
 FT VARIANT 473 473 T -> I.  
 FT CONFLICT 66 66 M -> K (IN REF. 2).  
 SQ SEQUENCE 656 AA; 74854 MW; ABB350B523879933 CRC64;  
 Query Match 14.8%; Score 87; DB 1; Length 656;  
 Best Local Similarity 30.9%; Pred. No. 0.23;  
 Matches 25; Conservative 15; Mismatches 31; Indels 10; Gaps 3;  
 Qy 21 ENVFPLR-----WKEFVIRGLSDHIDRLONGR-CLREAOYSMLATWRRRTPREA 73  
 Db 570 EHLNPIRENLGROWNCARKLGFTESQIDLDHIDYERDGLKERYQMLQKWLREGTKGA 629  
 Qy 74 TLELLGRVLRD---MDLLGL 91  
 Db 630 TVGKLAQALHCCCRIDLNLH 650  
 RESULT 10  
 ANKI MOUSE  
 ID ANKI\_MOUSE STANDARD; PRT; 1862 AA.  
 AC Q02357;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)







FT VARSPLIC 1512 1873 Missing (in isoform 2).  
 FT FTID=VSP\_000264.  
 FT H -> D (in isoform 2).  
 FT VARSPLIC 1874 1874  
 FT FTID=VSP\_000265.  
 FT TVEGLEDSSELEVDIYFMKSKDHTSTPNP -> ELRGS  
 FT GLOPDLIEGRKAQIVIRASLRKQKQ (in isoform  
 FT 3).  
 FT FTID=VSP\_000266.  
 FT R -> T.  
 FT FTID=VAR\_000595.  
 FT V -> I (in RS).  
 FT FTID=VAR\_000596.  
 FT R -> H (in Brueggen).  
 FT FTID=VAR\_000597.  
 FT V -> A.  
 FT FTID=VAR\_000598.  
 FT D -> E.  
 FT FTID=VAR\_000599.  
 FT E -> D.  
 FT FTID=VAR\_000601.  
 FT S -> T.  
 FT FTID=VAR\_000600.  
 FT D -> N (in Dueseldorf).  
 FT FTID=VAR\_000602.  
 FT R -> D.  
 FT FTID=VAR\_000603.  
 FT A -> S (in REF. 2).  
 FT CONFLICT 229 229  
 FT CONFLICT 1545 1545 V -> I (in REF. 2).  
 FT SEQUENCE 1880 AA; 206145 MW; 1C5F5E7EFDICD428 CRC64;  
 SQ

Query Match 13.1%; Score 77; DB 1; Length 1880;  
 Best Local Similarity 28.9%; Pred. No. 8.1;  
 Matches 24; Conservative 15; Mismatches 42; Indels 2; Gaps 2;

QY 5 POSLTDTPATL-YAVENVVPLRWKFKVRLGLSDHEIDRLQLNGRCLEAQAQSMLAT 63  
 DB 1393 PGSLSGTGEQMKMAVISEHLGLSWAEIARELQFSVEDINIRVENPNSLLEQSVALLNL 1452

QY 64 WRRTPRREATLELGRVLRDM 86  
 DB 1453 WIR-EGQVANMENLYTALQSD 1474

RESULT 14  
 ID T10B HUMAN STANDARD; PRT: 440 AA.  
 AC O14763; O14720; O15508; O15517; O15531; Q9BYE0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2003 (Rel. 40, Last sequence update)  
 DE Tumor necrosis factor receptor superfamily member 10B precursor (Death  
 DE receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL  
 DE receptor-2) (TRAIL-R2).  
 GN TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_TaxID=9606;  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF N-TERMINUS.  
 RC TISSUE=Forebrain fibroblast;  
 RX MEDLINE=97459925; PubMed=9311998;  
 RA Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y.,  
 RA Boiani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A.,  
 RA Goodwin R.G., Rauch C.T.;  
 RT "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";  
 RL EMBO J. 16:5386-5397(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), ALTERNATIVE  
 RP SPLICING, AND VARIANTS LEU-32 AND VAL-67.  
 RX MEDLINE=97431692; PubMed=9285725;  
 RA Screaton G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E.,  
 RA McMichael A.J., Bell J.I.;

RT "TRICK2, a new alternatively spliced receptor that transduces the  
 RT cytotoxic signal from TRAIL.";  
 RL Curr. Biol. 7:693-696(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), CHARACTERIZATION, AND VARIANTS  
 RP LEU-32 AND VAL-67.  
 RC TISSUE=Liver, and Spleen;  
 RX MEDLINE=98039016; PubMed=9373179;  
 RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,  
 RA Tachopp J.;  
 RT "Characterization of two receptors for TRAIL.";  
 RL FEBS Lett. 416:329-334(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RC TISSUE=Ovary;  
 RX MEDLINE=97467719; PubMed=9326928;  
 RA Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., Meng R.,  
 RA Krantz I.D., Kao J.D., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R.,  
 RA Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;  
 RT "KILLER/DR5 is a DNA damage-inducible p53-regulated death receptor  
 RT gene.";  
 RL Nat. Genet. 17:141-143(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RX MEDLINE=97390508; PubMed=9242610;  
 RA Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;  
 RT "An antagonist decoy receptor and a death domain-containing receptor  
 RT for TRAIL.";  
 RL Science 277:815-818(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.  
 RX MEDLINE=97467318; PubMed=9325248;  
 RA MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,  
 RA Cohen G.M., Alnemri E.S.;  
 RT "Identification and molecular cloning of two novel receptors for the  
 RT cytotoxic ligand TRAIL.";  
 RL J. Biol. Chem. 272:25417-25420(1997).  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.  
 RX MEDLINE=98090092; PubMed=9430227;  
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
 RT "Death receptor 5, a new member of the TNFR family, and DR4 induce  
 RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
 RL Immunity 7:821-830(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANT LEU-32.  
 RX MEDLINE=97390509; PubMed=9242611;  
 RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,  
 RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,  
 RA Goddard A.D., Godowski P., Ashkenazi A.;  
 RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy  
 RT receptors.";  
 RL Science 277:818-821(1997).  
 RN [9]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANTS LEU-32 AND VAL-67.  
 RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;  
 RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2  
 RT gene in colorectal carcinoma";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RX Cao X., Zhang W., Wan T.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.  
 RA Farrah T., Vu T., Gilbert T., Gross J., O'Hara P.;  
 RT "Homo sapiens homolog of tumor necrosis factor receptor.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT LEU-32.  
 RC TISSUE=Cervix;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,



Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Iqbalilano N.A., Peters G.J., Abramson R.D., Mullihy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W., Valladao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Feing J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [13]

X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183. MEDLINE=20017054; PubMed=10549288; Rymowitz S.G., Christinger H.W., Fuh G., Ullsch M., O'Connell M., Kelley R.F., Ashkenazi A., de Vos A.M.; "Friggiering cell death: the crystal structure of Apo2L/TRAIL in a complex with death receptor 5."; Mol. Cell 4:563-571 (1999). [14]

X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184. PubMed=10542098; Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I., Jones E.Y., Sreaton G.R.; "Structure of the TRAIL-DR5 complex reveals mechanisms conferring specificity in apoptotic initiation."; Nat. Struct. Biol. 6:1048-1053 (1999).

-I- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Promotes the activation of NF-kappaB.

-I- SUBUNIT: Homotrimer. Can interact with TRADD and RIP.

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2; Name=Long; Synonyms=TRICK2B; IsoId=014763-1; Sequence=displayed; Name=Short; Synonyms=TRICK2A; IsoId=014763-2; Sequence=VSP\_006490; -I- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues; very highly expressed in tumor cell lines such as HeLa S3, K562, HL-60, SW480, A549 and G361; highly expressed in heart, peripheral blood lymphocytes, liver, pancreas, spleen, thymus, prostate, ovary, uterus, placenta, testis, esophagus, stomach and throughout the intestinal tract; not detectable in brain.

-I- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.

-I- DISEASE: Defects in TNFRSF10B may be a cause of squamous cell carcinoma of the head and neck (HNSCC) [MIM:601400].

-I- SIMILARITY: Contains 3 TNFR-Cys repeats.

-I- SIMILARITY: Contains 1 death domain.

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EMBL; AF016849; AAC51778.1; -  
EMBL; AF018657; AAB70577.1; -  
EMBL; AF018658; AAB70578.1; -

```

RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.B. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Silveira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamine + tRNA(Gln) = AMP +
CC diphosphate + L-glutamyl-tRNA(Gln).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -----
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CC -----
DR EMBL; AE003966; AAF84147.1; -
DR PIR; G82693; G82693.
DR HSSP; P00962; LGTR.
DR HAMAP; MF_00126; -, 1.
DR InterPro; IPR004514; Glns.
DR InterPro; IPR000924; Glu tRNA-synt 1c.
DR InterPro; IPR001412; tRNA-synt I.
DR Pfam; PF00749; tRNA-synt 1c; 1.
DR Pfam; PF03950; tRNA-synt 1c; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR TIGRFAMs; TIGR00440; Glns; 1.
DR PROSITE; PS00178; AA tRNA LIGASE I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 41 51 "HIGH" REGION.
FT SITE 292 296 "KMSKS" REGION.
FT BINDING 295 295 ATP (BY SIMILARITY).
SQ SEQUENCE 580 AA; 66293 MW; B9013A4D6630C16D CRC64;
Query Match 12.5%; Score 73.5; DB 1; Length 580;
Best Local Similarity 33.0%; Pred. No. 5.1;
Matches 32; Conservative 12; Mismatches 32; Indels 21; Gaps 6;
QY 11 DDPATLYAVV-----ENVPPLRWKFEVXRLGLSDHE--IDRLQLNGRCIREAQYMLATW 64
Db ||| : : : : : : : : : : : : : : : : : : : :
311 DDP-RMYTLQGLRRRGYTPAAMRLFVERIGISKQNSIIDFSVLEN--CLRENLDTI----- 363
QY 65 RRTFRRENTLELLGRVLDMDLLGCLDEDIEALCP 101
Db ||| : : : : : : : : : : : : : : : : : : : :
364 ---APPRMATIAPLXIVLTNLP-----EDHEQLIFF 392

```

Search completed: June 1, 2004, 14:44:28  
Job time : 10.0479 secs

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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:35:21 ; Search time 33.5329 Seconds  
(without alignments)  
1053.831 Million cell updates/sec

Title: US-09-854-906-1

Perfect score: 587

Sequence: 1 MAHKPSLTDTPATLYAVV.....DIEALCGPAALPPAPSLR 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phage.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_unclassified.\*

14: sp\_rvirus.\*

15: sp\_bacteriaph.\*

16: sp\_bacteriaph.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	474.5	80.8	446	Q95ND3	Q95nd3 felis silve
2	155	26.4	387	Q8VD70	Q8vd70 mus musculu
3	149	25.4	413	Q99MM1	Q99mm1 mus musculu
4	83	14.1	410	Q7T3M8	Q7t3m8 gallus gall
5	83	14.1	1848	Q1G1302	Q1g1302 mus musculu
6	82.5	14.1	365	Q81645	Q81645 hepatitis c
7	82.5	14.1	3011	Q913D4	Q913d4 hepatitis c
8	82	14.0	163	Q9YBB1	Q9ybb1 atropyrum p
9	81.5	13.9	364	Q86797	Q86797 hepatitis c
10	81.5	13.9	365	Q81652	Q81652 hepatitis c
11	81.5	13.9	634	Q8STZ1	Q8stz1 encephalito
12	81.5	13.9	3011	Q81754	Q81754 hepatitis c
13	81.5	13.9	3022	Q86798	Q86798 hepatitis c
14	80.5	13.7	368	Q87408	Q87408 melesgris g
15	80	13.6	273	Q9V6H5	Q9v6h5 drosophila
16	79.5	13.5	634	Q8ST44	Q8st44 encephalito

#### ALIGNMENTS

RESULT 1

Q95ND3 PRELIMINARY; PRT; 446 AA.

AC Q95ND3; DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Tumor necrosis factor type I.

GN TNFR I.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI\_TaxID=9685;

RN [1]

RP SEQUENCE FROM N.A.

RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;

RT "Molecular cloning of feline tumor necrosis factor receptor type I

(TNFR I ) and expression of TNFR I and TNFR II in various disease in

cats.,"

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB051103; BAB55455.1; "

DR GO; GO:0005489; P:electron transporter activity; IEA.

DR GO; GO:0004872; R:receptor activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR000345; CytC\_heme\_BS.

DR InterPro; IPR000488; Death.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00020; TNFR\_c6; 4.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00190; CYTOCHROME C; 1.

DR PROSITE; PS00017; DEATH\_DOMAIN; 1.

DR PROSITE; PS01186; EGF\_2; 1.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.

DR PROSITE; PS00500; TNFR\_NGFR\_2; 3.

DR SEQUENCE 446 AA; 49563 MW; 217BD331DD8A74AA CRC64;

17 79 13.5 143 11 070510  
18 79 13.5 960 11 08VDA0  
19 78 13.3 626 16 09KYP5  
20 77.5 13.2 314 6 0861W6  
21 77.5 13.2 838 11 09QXHI  
22 77.5 13.2 1093 11 08CBN3  
23 77.5 13.2 1726 11 08VC68  
24 77.5 13.2 1762 11 088521  
25 77.5 13.2 1887 4 0723G4  
26 77.5 13.2 1943 11 061307  
27 77.5 13.2 2622 11 070511  
28 77 13.1 316 16 09HXZ2  
29 77 13.1 1038 11 080ZZ7  
30 77 13.1 1050 11 08CCV0  
31 77 13.1 1719 4 013768  
32 77 13.1 1856 4 099407  
33 76.5 13.0 364 12 068824  
34 76.5 13.0 364 12 068805  
35 76.5 13.0 388 16 097PS5  
36 76 12.9 303 5 09NHG0  
37 76 12.9 536 16 0912T7  
38 76 12.9 965 4 072344  
39 76 12.9 1863 4 0723L5  
40 75.5 12.9 319 6 09TV79  
41 75.5 12.9 320 6 09XS29  
42 75.5 12.9 356 10 08GRN3  
43 75.5 12.9 364 12 092543  
44 75.5 12.9 364 12 092538  
45 75.5 12.9 811 4 09H0P5

O70510 rattus norv  
Q8vda0 rattus norv  
Q9kyp5 streptomyc  
Q861w6 felis silve  
Q9qxi1 mus musculu  
Q8cbn3 mus musculu  
Q8vc68 mus musculu  
O88521 rattus norv  
Q723g4 homo sapien  
Q61307 mus musculu  
O70511 rattus norv  
Q9hxx2 pseudomonas  
Q80zz7 mus musculu  
Q8ccv0 mus musculu  
Q13768 homo sapien  
Q99407 homo sapien  
Q68824 hepatitis c  
Q68805 hepatitis c  
Q97ps5 streptococ  
Q9nhg0 drosophila  
Q912t7 pseudomonas  
Q72344 homo sapien  
Q723l5 homo sapien  
Q9tv79 oryctolagus  
Q9xs29 oryctolagus  
Q8grn3 oryza sativ  
Q92543 hepatitis c  
O92538 hepatitis c  
Q9h0p5 homo sapien

```
Query Match      80.8%; Score 474.5; DB 6; Length 446;
Best Local Similarity 83.5%; Pred. No. 5.8e-42;
Matches 91; Conservative 8; Mismatches 9; Indels 1; Gaps 1;

QY 4 KPQSLDTPDPTLYAVVENPPLRWKFEVKRLGSLDHEIDRLQLNGRCLEAQAQYMLAT 63
Db RPEA-DPADPTLYAVDVGVPSPRWKFEVRLGLSEHIEIRLELQNGRCLEAHYMLAA 397

QY 64 WRRRTPREATLELGRVLRDMDLLGCLDIEEALCGPAALPPAPSLIR 112
Db WRRRTPREATLELGRVLRDMDLLGCLDIEEALCAPASLSPAPRLIR 446

RESULT 2
Q3VD70 ID Q8VD70 PRELIMINARY; PRT; 387 AA.
AC Q8VD70;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 12.
GN TNFRSF25 OR TNFRSF12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017526; AAH17526.1; -.
DR MGD; MGI:1934667; Tnfrsf25.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00505; TNFR_NGFR_2; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 387 AA; 41640 MW; F16644666BAD68D3 CRC64;

Query Match      26.4%; Score 155; DB 11; Length 387;
Best Local Similarity 43.4%; Pred. No. 4.1e-08;
Matches 36; Conservative 13; Mismatches 30; Indels 4; Gaps 2;

QY 16 LYAVVENPPLRWKFEVKRLGSLDHEIDRLQLNGRCLEAQAQYMLATWRRTTPREATL 75
Db 305 LYDVMDAVPARRWKEFVRLTGLREAEI EAVEVEICR-FRDOQYEMLKRWROQQP---AGL 360

QY 76 ELLGRVLRDMDLLGCLDIEEAL 98
Db 361 GAIIYAALERKLGCAEDLSRL 383

RESULT 3
Q39MM1 ID Q99MM1 PRELIMINARY; PRT; 413 AA.
AC Q99MM1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE WSL-1-like protein.
GN TNFRSF25 OR TNFRSF12.
OS Mus musculus (Mouse).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=21158384; PubMed=11261933;
RA Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
RA Owen M.J.;
RT "Genomic structure, expression, and chromosome mapping of the mouse
RT homologue for the WSL-1 (DR3, Apo3, TRAMP, IARD, TR3, TNFRSF12)
RT gene.";
RL Immunogenetics 53:59-63(2001).
DR EMBL; AF329969; AAK11256.1; -.
DR HSSP; Q92956; IJWA.
DR MGD; MGI:1934667; Tnfrsf25.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00505; TNFR_NGFR_2; 1.
DR SEQUENCE 413 AA; 44453 MW; 69F21B85D0DABABF CRC64;

Query Match      25.4%; Score 149; DB 11; Length 413;
Best Local Similarity 42.2%; Pred. No. 1.9e-07;
Matches 35; Conservative 13; Mismatches 31; Indels 4; Gaps 2;

QY 16 LYAVVENPPLRWKFEVKRLGSLDHEIDRLQLNGRCLEAQAQYMLATWRRTTPREATL 75
Db 331 LYDVMDAVPARRWKEFVRLTGLREAEI EAVEVEICR-FRDOQYEMLKRWROQQP---AGL 386

QY 76 ELLGRVLRDMDLLGCLDIEEAL 98
Db 387 GAIIYAALERKLGCAEDLSRL 409

RESULT 4
Q7T3M8 ID Q7T3M8 PRELIMINARY; PRT; 410 AA.
AC Q7T3M8;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Death domain-containing tumor necrosis factor receptor superfamily
DE member 23 variant 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgham J.T., Johnson A.L.;
RT "Identification and characterization of alternatively spliced, ovarian
RT enhanced death receptor and decoy receptor.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251408; AAP41833.1; -.
KW Receptor.
FT NON TER 410 410
SQ SEQUENCE 410 AA; 46194 MW; 4BFC7C7016C2BA60 CRC64;

Query Match      14.1%; Score 83; DB 13; Length 410;
Best Local Similarity 25.7%; Pred. No. 1.9;
Matches 18; Conservative 21; Mismatches 29; Indels 2; Gaps 2;
```

RESULT 6  
Q81645  
ID Q81645 PRELIMINARY; PRT; 365 AA.

-1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA (BY SIMILARITY).

35

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DR EMBL: AY051292; AAK95832.1; -.
DR MEROPS; S29.001; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.
DR GO; GO:0003489; F:electron transporter activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV NS2.
DR InterPro; IPR002518; HCV NS3.
DR InterPro; IPR000745; HCV NS4a.
DR InterPro; IPR001490; HCV NS4b.
DR InterPro; IPR002868; HCV NS5a.
DR InterPro; IPR002166; HCV RdRp.
DR InterPro; IPR004109; Peptidase C29.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
DR Pfam; PF01539; HCV env; 1.
DR Pfam; PF01560; HCV NS1; 1.
DR Pfam; PF01538; HCV NS2; 1.
DR Pfam; PF02907; HCV NS3; 1.
DR Pfam; PF01006; HCV NS4a; 1.
DR Pfam; PF01001; HCV NS4b; 1.
DR Pfam; PF01506; HCV NS5a; 1.
DR Pfam; PF00998; Viral RdRp; 1.
DR ProDom; PD186062; HCV NS1; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME C; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.
SQ SEQUENCE 3011 AA; 327234 MW; 57A21964B4227B60 CRC64;

Query Match 14.1%; Score 82.5; DB 12; Length 3011;
Best Local Similarity 26.0%; Pred. No. 21;
Matches 33; Conservative 13; Mismatches 40; Indels 41; Gaps 5;

QY 3 HKPQSLDTPDDPATYAVVENVPPLEKKEFVKEL-----GLSDHIDRLQLNGRCL 53
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2858 HLGKALDCE----YGVAVHSVQPLDPLPIQLHSLSAFSLHSYSPGEINRV-----AAAL 2909

QY 54 REAQYSLMATRRRPPREATLELGRVLRMDMLGCLDEALCG-----FAA 103
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2910 RKLGVPLPRAWHRARSVRATLLSOGG-----KAAICGKYLEFNWAVTKLK 2955

QY 104 LPPAPSL 110
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2956 LTPLEPSM 2962

RESULT 8
QYIB1
ID Q9YBB1 PRELIMINARY; PRT; 163 AA.
AC Q9YBB1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)

101-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
163AA long hypothetical methylmalonyl-CoA mutase alpha-subunit.
APE1686.
Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
NCBI_TaxID=56636;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000062; BAA80687.1; -.
DR PIR; B72550; B72550.
DR HSP; P11653; IRSQ.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR InterPro; IPR006159; Acid CoA mut C.
DR InterPro; IPR006158; B12-Binding.
DR Pfam; PF02310; B12-binding; 1.
DR TIGRFAMs; TIGR00640; acid_CoA_mut_C; 1.
KW Complete proteome.
SQ SEQUENCE 163 AA; 17969 MW; C0BD5F04FEEFD4A6 CRC64;

Query Match 14.0%; Score 82; DB 17; Length 163;
Best Local Similarity 32.9%; Pred. No. 0.88;
Matches 23; Conservative 13; Mismatches 28; Indels 6; Gaps 2;

QY 20 VENVPPLRWKEFVKRLGSLSDHIDRLQLNGRCLREAQYSLMATRRRTPREATLEL 79
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
13 VLGTPLRRYKVLVAKMGLDGH--DRGAKVVARALRDAGFEVVTGLRQTPEQVA----MA 66

QY 80 RVLDRMDLLG 89
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
67 AVQEDVDVIG 76

RESULT 9
Q68797 PRELIMINARY; PRT; 364 AA.
AC Q68797;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NS5 (Genome polyprotein) (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
ON NCBI_TaxID=11103;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JK046;
RX MEDLINE=96226020; PubMed=8627233;
RA Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F.,
RA Lesmana L.A., Miyakawa Y., Mayumi M.;
RT "Hepatitis C virus variants from Jakarta, Indonesia classifiable into
novel genotypes in the second (2e and 2f), tenth (10a) and eleventh
(11a) genetic groups.";
RL J. Gen. Virol. 77:293-301(1996).
DR EMBL; D49763; BAA08597.1; -.
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.

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QY 104 LPPAPS 109
Db 310 LTELPS 315

RESULT 11
Q8STZL Q8STZL PRELIMINARY; PRT; 634 AA.
AC Q8STZ1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein ECU11_2090.
GN ECU11 2090.
OS Encephalitozoon cuniculi.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OC NCBI_TaxID=6035;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat P.,
RA Prensier G., Barbe V., Peyretallade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weisenbach J., Vivares C.P.;
RA "genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453 (2001).
RW EMBL; AL590450; CAD26119.1; -.
KW Hypothetical protein.
SQ SEQUENCE 634 AA; 74611 MW; D326957544285663 CRC64;

Query Match 13.9%; Score 81.5; DB 5; Length 634;
Best Local Similarity 29.5%; Pred. No. 4.6;
Matches 28; Conservative 15; Mismatches 41; Indels 11; Gaps 3;

QY 5 PQSLDTDDPATLYAVVENVPPLRWKEFVVRGLSLSHEDIRLQNGRCRLREAOYSMLATW 64
Db 187 PQSLSEDERRRREVMILQRV-----KEYGRLMCTEDKQKEIVEAQKIMCDACEQ-----IW 236
QY 65 RRRTPREATLELLGRVLRMDMLIGCLE-DIREAL 98
Db 237 RREDRKEFTMEIYSRYLNKVMRGVGRVEDPL 271

RESULT 12
Q81754 Q81754 PRELIMINARY; PRT; 3011 AA.
AC Q81754;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Genome polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=111103;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=HC-G9;
RA Okamoto H.;
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=HC-G9;
RX MEDLINE=94172337; PubMed=8126459;
RA Okamoto H., Kojima M., Sakamoto M., Tizuka H., Hadiwandowo S.,
RA Suwignyo S., Miyakawa Y., Mayumi M.;

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"The entire nucleotide sequence and classification of a hepatitis C virus isolate of a novel genotype from an Indonesian patient with chronic liver disease."

J. Gen. Virol. 75:629-635(1994).

!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA (BY SIMILARITY).

EMBL; D14853; BAA03581.1; -.

PIR; PQ0804; PQ0804.

HSSP; P26663; LJXP.

MEROFS; S29.001; -.

MEROFS; U39.001; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0008026; F:ATP dependent helicase activity; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0008236; F:serine-type peptidase activity; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0008508; F:proteolysis and peptidolysis; IEA.

GO; GO:0006350; F:proteolysis and peptidolysis; IEA.

GO; GO:0019079; P:viral genome replication; IEA.

GO; GO:0013087; P:viral genome replication; IEA.

InterPro; IPR009003; Cys Ser\_trypsin.

InterPro; IPR001410; DEAD.

InterPro; IPR002522; HCV\_capsid.

InterPro; IPR002521; HCV env.

InterPro; IPR002519; HCV NS1.

InterPro; IPR002531; HCV NS2.

InterPro; IPR002518; HCV NS3.

InterPro; IPR000745; HCV NS4a.

InterPro; IPR001490; HCV NS4b.

InterPro; IPR002868; HCV NS5a.

InterPro; IPR002166; HCV RdRp.

InterPro; IPR004109; Peptidase C29.

InterPro; IPR007095; RNA\_pol DS\_PS.

InterPro; IPR007094; RNA\_pol\_PStr.

Pfam; PF01543; HCV\_capsid; 1.

Pfam; PF01542; HCV\_core; 1.

Pfam; PF01539; HCV env; 1.

Pfam; PF01560; HCV NS1; 1.

Pfam; PF01538; HCV NS2; 1.

Pfam; PF02907; HCV NS3; 1.

Pfam; PF01006; HCV NS4a; 1.

Pfam; PF01001; HCV NS4b; 1.

Pfam; PF01506; HCV NS5a; 1.

Pfam; PF00998; Viral RdRp; 1.

ProDom; PD186062; HCV NS1; 1.

SMART; SM00487; DRXDC; 1.

Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.

CHAIN 1 191

CHAIN 192 383

CHAIN 384 809

CHAIN 810 1006

CHAIN 1007 1657

CHAIN 1658 1972

CHAIN 1973 3011

SEQUENCE 3011 AA; 327212 MW; 9C16C120F4E79268 CRC64;

Query Match 13.9%; Score 81.5; DB 12; Length 3011;

Best Local Similarity 27.8%; Pred.No. 26;

Matches 35; Conservative 11; Mismatches 39; Indels 41; Gaps 6;

3 HKPQSLDTPDPAFLYAVNVPFLRKFVKGL-GL-----SPHEIDRLQLNGRCL 53

2858 HLEKALDCE---IYGAVHSVQPLDPLPIQLRHLGLSAPLSHSYSPGEINRV-----AACL 2909

54 REAQSYMLATWRRTRPRTEATLELGRVDRMDLLGCLLEDEALCG-----PAA 103

Db 2910 RKLGVPLRAWHRARSVRATILSQG-----RAAICGKYLENNVAKTKLK 2955

QY 104 LPPAPS 109

Db 2956 LTPPLPS 2961

RESULT 13

Q68798 PRELIMINARY; PRT; 3022 AA.

ID Q68798

AC Q68798; 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Genome polyprotein.

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI\_TaxID=111103;

RN [1]\_SEQUENCE FROM N.A.

RC STRAIN-JK046;

RX MEDLINE=962226020; PubMed=8627233;

RA Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tada F.,

RA Lesmana L.A., Miyakawa Y., Mayumi M.,

RT "Hepatitis C virus variants from Jakarta, Indonesia classifiable into

RT novel genotypes in the second (2e and 2f), tenth (10a) and eleventh

RT (11a) genetic groups.";

RL J. Gen. Virol. 77:293-301(1996).

CC !- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A

CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:

CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF

CC PROTEIN C AND MRNA (BY SIMILARITY).

DR EMBL; D63822; BAA09891.1; -.

DR HSSP; P27958; IHET.

DR MEROFS; S29.001; -.

DR MEROFS; U39.001; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.

DR GO; GO:0003723; F:RNA binding; IEA.

DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

DR GO; GO:0008236; F:serine-type peptidase activity; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.

DR GO; GO:0006350; F:proteolysis and peptidolysis; IEA.

DR GO; GO:0019079; P:viral genome replication; IEA.

DR GO; GO:0019087; P:viral genome replication; IEA.

DR InterPro; IPR009003; Cys Ser\_trypsin.

DR InterPro; IPR001410; DEAD.

DR InterPro; IPR002522; HCV capsid.

DR InterPro; IPR002521; HCV core.

DR InterPro; IPR002519; HCV env.

DR InterPro; IPR002531; HCV NS1.

DR InterPro; IPR002518; HCV NS2.

DR InterPro; IPR000745; HCV NS4a.

DR InterPro; IPR001490; HCV NS4b.

DR InterPro; IPR002868; HCV NS5a.

DR InterPro; IPR002166; HCV RdRp.

DR InterPro; IPR004109; Peptidase C29.

DR InterPro; IPR007095; RNA\_pol DS\_PS.

DR InterPro; IPR007094; RNA\_pol\_PStr.

DR Pfam; PF01543; HCV\_capsid; 1.

DR Pfam; PF01542; HCV\_core; 1.

DR Pfam; PF01539; HCV env; 1.

DR Pfam; PF01560; HCV NS1; 1.

DR Pfam; PF01538; HCV NS2; 1.

DR Pfam; PF02907; HCV NS3; 1.

DR Pfam; PF01006; HCV NS4a; 1.



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DR Pfam; PF01001; HCV NS4b; 1.
DR Pfam; PF01506; HCV NS5a; 1.
DR Pfam; PF00998; Viral RdRP; 1.
DR ProDom; PD186062; HCV NS1; 1.
DR SMART; SM00487; DEXDC; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.
SQ SEQUENCE 3022 AA; 328683 MW; EEGA21538FEA26E1 CRC64;

Query Match 13.9%; Score 81.5; DB 12; Length 3022;
Best Local Similarity 28.0%; Pred. No. 26;
Matches 30; Conservative 12; Mismatches 32; Indels 33; Gaps 5;

QY 3 HKPQSLDTPATLYAVENVPLRWKFEVKRL-----GLSDHEIDRLQLNGRCGL 53
DB 2871 HK--ALDFD---MYGVYNTITLDTLQIQLHGMMAFSLHGVSPELNRV-----GACL 2920

QY 54 REAQYSLATWTRTPREATLELLGRVLRMDLLGLCLDIEALCG 100
DB 2921 RKLGAFLRAWRHRARAVRAKLIAQGG-----KAAICG 2953

RESULT 14
OS7408 PRELIMINARY; PRT; 368 AA.
AC OS7408;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Subgroup E ALV receptor.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97471016; PubMed=9326659;
RA Adkins H.B.; Brojatsch J.; Naughton J.; Rolls M.M.; Pesola J.M.;
RA Young J.A.;
RT "Identification of a cellular receptor for subgroup E avian leukosis
virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11617-11622 (1997).
DR EMBL; AF060002; AAB99987.1; -.
DR HSSP; O14763; 1D0G.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0004872; F:electron transporter activity; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; Ribosomal_S2.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
DR PROSITE; PS00117; DEATH DOMAIN; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 368 AA; 41020 MW; 5701AC2A6D4F87E2 CRC64;

Query Match 13.7%; Score 80.5; DB 13; Length 368;
Best Local Similarity 29.3%; Pred. No. 3; 2;
Matches 27; Conservative 16; Mismatches 42; Indels 7; Gaps 3;

QY 12 DPATLYA-----VVENVPPLRWKFEVKRLGLSDHEIDRLQLNGRCLEAQYSLATWTR 66
```

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Db 268 DPITVLISSSNTFVDLVFPQWRFRGALGRNNLYQAE-QNDRESGEPLQMLIMLN 326
QY 67 RTPREATLELLGRVLRMDLLGLCLDIEAL 98
Db 327 KEGSK-ASVNTLTLETLSQISLSGVADIASEL 357

RESULT 15
Q9V8H5 PRELIMINARY; PRT; 273 AA.
AC Q9V8H5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG5576 protein (GH20785P).
GN IMD OR CG5576.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D.; Celnik S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.;
RA Amanatides P.G.; Scherer S.E.; Li P.W.; Hoskins R.A.; Galle R.F.;
RA George R.A.; Lewis S.E.; Richards S.; Ashburner M.; Henderson S.N.;
RA Sutton G.G.; Wortman J.R.; Yandell M.D.; Zhang Q.; Chen L.X.;
RA Brandon R.C.; Rogers Y.-H.C.; Blazej R.G.; Champe M.; Pfeiffer B.D.;
RA Wan K.H.; Doyle C.; Baxter E.G.; Helt G.; Nelson C.R.; Miklos G.L.G.;
RA Abriel J.F.; Agbayani A.; An H.-J.; Andrews-Frankoch C.; Baldwin D.;
RA Ballew R.M.; Basu A.; Baxendale J.; Bayraktaroglu L.; Beasley E.M.;
RA Beeson K.Y.; Benos P.V.; Berman B.P.; Bhandari D.; Boldakov S.;
RA Borkova D.; Botchan M.R.; Bouck J.; Brokstein P.; Bottier P.;
RA Burtis K.C.; Busam D.A.; Butler H.; Cadieu E.; Center A.; Chandra I.;
RA Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.;
RA de Pablos B.; Delcher A.; Deng Z.; Mays A.D.; Dew I.; Dietz S.M.;
RA Dodson K.; Doup L.E.; Downes M.; Dugan-Rocha S.; Dunkov B.C.; Dunn P.;
RA Durbin K.J.; Evangelista C.C.; Ferraz C.; Kravitz S.; Kulp D.; Lai Z.;
RA Foster C.; Gabriellian A.E.; Garg N.S.; Gelbart W.M.; Glasser K.;
RA Glodek A.; Gong F.; Gorrell J.H.; Gu Z.; Guan P.; Harris M.;
RA Harris N.L.; Harvey D.; Heiman T.J.; Hernandez J.R.; Houck J.;
RA Hoskin D.; Houston K.A.; Howland T.J.; Wei M.-H.; Ibegwam C.;
RA Jalali M.; Kalush F.; Karpen G.H.; Ke Z.; Kennison J.A.; Ketchum K.A.;
RA Kimmel B.E.; Kodira C.D.; Kraft C.; Kravitz S.; Kulp D.; Lai Z.;
RA Lasko P.; Lei Y.; Levitsky A.A.; Li J.; Li Z.; Liang Y.; Lin X.;
RA Liu X.; Mattei B.; McIntosh T.C.; McLeod M.P.; McPherson D.;
RA Merkulov G.; Milehina N.V.; Mobarry C.; Morris J.; Moshrefi A.;
RA Mount S.M.; Moy M.; Murphy B.; Murphy L.; Muzny D.M.; Nelson D.L.;
RA Nelson D.R.; Nelson K.A.; Nixon K.; Nusskern D.R.; Pacleb J.M.;
RA Palazzolo M.; Pittman G.S.; Pan S.; Pollard J.; Puri V.; Reese M.G.;
RA Reinert K.; Remington K.; Saunders R.D.C.; Scheeler F.; Shen H.;
RA Shue B.C.; Siden-Kiamos I.; Simpson M.; Skupski M.P.; Smith T.;
RA Spier E.; Spradling A.C.; Stapleton M.; Strong R.; Sun E.;
RA Svirskas R.; Tector C.; Turner R.; Venter E.; Wang A.H.; Wang X.;
RA Wang Z.-Y.; Wassarman D.A.; Weinstein G.M.; Weissbach J.;
RA Williams S.M.; Woodage T.; Worley K.C.; Wu D.; Yang S.; Yao Q.A.;
RA Ye J.; Yeh R.-F.; Zaveri J.S.; Zhan M.; Zhang G.; Zhao Q.; Zheng L.;
RA Zheng X.H.; Zhong F.N.; Zhong W.; Zhou X.; Zhu S.; Zhu X.; Smith H.O.;
Gibbs R.A.; Myers E.W.; Rubin G.M.; Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley.
RA Stapleton M.; Brokstein P.; Hong L.; Agbayani A.; Carlson J.;
RA Champe M.; Chavez C.; Dorsett V.; Farfan D.; Frise E.; George R.;
RA Gonzalez M.; Guarin H.; Li P.; Liao G.; Miranda A.; Mungall C.J.;
RA Nunoo J.; Pacleb J.; Paragas V.; Park S.; Phouanavong S.; Wan K.;
RA Yu C.; Lewis S.E.; Rubin G.M.; Celnik S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
```

DR EMBL; AB003799; AAF57692.1; -.  
DR EMBL; AY051558; AAK2982.1; -.  
DR FlyBase; FBgn0013983; imd.  
DR GO; GO:0008961; P:antibacterial humoral response (sensu Inver. . .; IMP.  
DR GO; GO:0008963; P:antibacterial polypeptide induction; IMP.  
DR GO; GO:0006959; P:humoral immune response; IMP.  
DR InterPro; IPR000488; Death.  
DR Pfam; PF0531; death; 1.  
DR PROSITE; PS50017; DEATH DOMAIN; 1.  
SQ SEQUENCE 273 AA; 29899 MW; 7247CA4B46F5545B CRC64;  
  
Query Match 13.6%; Score 80; DB 5; Length 273;  
Best Local Similarity 23.8%; Pred. No. 2.6;  
Matches 25; Conservative 26; Mismatches 38; Indels 16; Gaps 3;  
  
QY 4 KPQSLDTPATLYAVVEN--VPPLR-----WKEFVKRLGLSDHEIDR--LEL 47  
Db 153 KPRASATRTVSIIVAMQSQEEDVRLLDVSTHGLGKWKQVNRDLGMSGEQIDQAIIDH 212  
  
QY 48 QNGRCILREAQYSMLATWRRTTPRRATLELLGRVLRDMDLLGCL 92  
Db 213 QMHGNIREVYIQLLQWIRSSADGVATVGRLTLLWESQHRDCVQ 257

Search completed: June 1, 2004, 14:46:20  
Job time : 34.5329 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:30:06 ; Search time 48.521 Seconds  
(without alignments)  
646.376 Million cell updates/sec

Title: US-09-854-906-8

Perfect score: 582

Sequence: 1 AHRPQLDTPATLYAVVE.....DIEALCGPAALPPAPSLLR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Genesep\_29Jan04:\*  
1: Genesep1980s:\*  
2: Genesep1990s:\*  
3: Genesep2000s:\*  
4: Genesep2001s:\*  
5: Genesep2002s:\*  
6: Genesep2003as:\*  
7: Genesep2003bs:\*  
8: Genesep2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	582	100.0	111	5 ABB81749	Abb81749 Tumour ne
2	582	100.0	158	5 ABG70127	Abg70127 Human pre
3	582	100.0	426	7 ABW00828	Abw00828 Human p55
4	582	100.0	453	4 AAB50895	Aab50895 Human TNF
5	582	100.0	455	2 ABG74755	Abg74755 Human TNF
6	582	100.0	455	2 AAR07451	Aar07451 Human tum
7	582	100.0	455	2 ABG74751	Abg74751 Human TNF
8	582	100.0	455	2 AAR12550	Aar12550 Type I TN
9	582	100.0	455	2 AAR10986	Aar10986 30kD TNF
10	582	100.0	455	2 AAR11082	Aar11082 Human 55k
11	582	100.0	455	2 AAR20787	Aar20787 TNF-alpha
12	582	100.0	455	2 AAR42059	Aar42059 Lambda de
13	582	100.0	455	2 AAR51034	Aar51034 Mutant p5
14	582	100.0	455	2 AAR42197	Aar42197 p55 Tumou
15	582	100.0	455	2 AAR75084	Aar75084 p55 TNF-R
16	582	100.0	455	2 AAY30934	Aay30934 Human tum
17	582	100.0	455	3 AAB01336	Aab01336 TNF-RI de
18	582	100.0	455	3 AAB26984	Aab26984 Human TNF
19	582	100.0	455	3 AAB36266	Aab36266 Human tum
20	582	100.0	455	3 AAB23446	Aab23446 Human tum
21	582	100.0	455	3 AAB37800	Aab37800 Human tum
22	582	100.0	455	4 AAB86817	Aab86817 Human TNF
23	582	100.0	455	4 AAB37677	Aab37677 Human 30
24	582	100.0	455	4 AAB36697	Aab36697 Human tum
25	582	100.0	455	5 AAU75064	Aau75064 Human tum

26	582	100.0	455	5 AAO22286	Aao22286 TNFR1 exp
27	582	100.0	455	5 ABB81649	Abb81649 Human tum
28	582	100.0	455	5 ABP54799	Abp54799 Human COP
29	582	100.0	455	6 ABP70914	Abp70914 Human CON
30	582	100.0	455	6 ABR58539	AbR58539 Human tum
31	582	100.0	455	6 ADA20581	Ada20581 Precursor
32	582	100.0	455	7 ADE57929	AdE57929 Human Pro
33	582	100.0	909	2 AAW64485	Aaw64485 Human Pas
34	579	99.5	112	5 ABB81751	Abb81751 Tumour ne
35	557	95.7	455	2 AAR24000	Aar24000 TNF-alpha
36	521	89.5	443	2 AAR51033	Aar51033 Mutant p5
37	469	80.6	433	2 AAR51032	Aar51032 Mutant p5
38	446	76.6	86	4 AAY97655	Aay97655 Human TNF
39	446	76.6	108	2 AAW73570	Aaw73570 Cytoplas
40	424	72.9	471	5 ABB98169	Abb98169 Bovine tu
41	424	72.9	471	5 AAE25816	Aae25816 Bovine tu
42	407	69.9	78	5 ABG31493	Abg31493 Human Apo
43	407	69.9	78	6 ADA49709	Ada49709 Death dom
44	397.5	68.3	84	2 AAW62179	Aaw62179 Tumour ne
45	386	66.3	461	2 ABG74754	Abg74754 Rat TNF-R

ALIGNMENTS

RESULT 1  
ABB81749  
ID ABB81749 standard; protein; 111 AA.  
AC ABB81749;  
XX  
XX  
10-SEP-2002 (first entry)  
XX  
DE Tumour necrosis factor receptor 1 death domain (shorter sequence).  
XX  
KW Tumour necrosis factor receptor 1; receptor; TNFR-1; death domain;  
XX receptor signalling; TNFR-1 DD; protein co-ordinate data.  
XX  
OS Unidentified.

Key	Location/Qualifiers
FT Region	15..21
FT Region	/label= Alpha_helix_1
FT Region	28..34
FT Region	/label= Alpha_helix_2
FT Region	38..42
FT Region	/label= Alpha_helix_3
FT Region	52..65
FT Region	/label= Alpha_helix_4
FT Region	72..85
FT Region	/label= Alpha_helix_5
FT Region	89..98
FT Region	/label= Alpha_helix_6

US2002045578-A1.

18-APR-2002.

14-MAY-2001; 2001US-00854906.

22-MAY-2000; 2000US-0206215P.

(SUKI/) SUKITS S F.

(XUGG/) XU G.

(LNU/) LTN J.

(TELL/) TELLIEZ J.

(HSUS/) HSU S.

Sukits SF, Xu G, Lin L, Telliez J, Hsu S;

WPI; 2002-443412/47.

PT Solution comprising tumor necrosis factor receptor 1 death domain, useful

PT for identifying potential inhibitor of tumor necrosis factor receptor 1  
 PT death domain.  
 PS Claim 1; Fig 4; 49pp; English.  
 XX  
 CC The sequence represents the tumour necrosis factor receptor 1 death  
 CC domain (TNFR-1 DD), which is the intracellular functional domain  
 CC responsible for the receptor signalling activities. The invention relates  
 CC to a novel solution comprising a tumour necrosis factor receptor 1 death  
 CC domain. The solution is useful for identifying a potential inhibitor of  
 CC TNFR-1 DD, for the design and selection of potent and selective  
 CC inhibitors of TNF signalling pathways, and for generating a three-  
 CC dimensional structure for an unknown molecule or molecular complex  
 XX  
 SX Sequence 111 AA;

Query Match 100.0%; Score 582; DB 5; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AHKPSLTDTPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQLNGRCCLREAQYSML 60  
 DB 1 AHKPSLTDTPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQLNGRCCLREAQYSML 60  
 QY 61 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 111  
 DB 61 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 111

RESULT 2  
 ABG70127  
 ID ABG70127 standard; protein; 158 AA.  
 XX  
 AC ABG70127;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Human prey protein for Shigella ipaB #4.  
 XX  
 KW Prey protein; ospB; ospD; ipaB; ipaC; ipaH9.8; ospG; ospC1; Shigella;  
 KW shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid system;  
 KW protein-protein interaction; SID; selected interacting domain; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200257303-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 11-JAN-2002; 2002WO-EP000777.  
 XX  
 PR 12-JAN-2001; 2001US-0261130P.  
 XX  
 PA (HYBR-) HYBRIGENICS.  
 XX  
 PI Legrain P;  
 XX  
 DR WPI; 2002-599706/64.  
 DR N-PSDB; ABS51520.  
 XX

XX New complex of protein-protein interactions between a bait Shigella  
 PT flexneri polypeptide and a prey mammalian or human placenta polypeptide  
 PT for treating or preventing bacillary dysentery in a mammal or human.  
 XX  
 PS Claim 7; Page 94; 162pp; English.

XX The invention relates to a complex of protein-protein interactions  
 CC between a Shigella flexneri polypeptide (e.g. ospB, ospD1, ipaB, ipaC,  
 CC ipaH9.8, ospG and ospC1) and a mammalian polypeptide defined in the  
 CC specification. The complexes are formed using the yeast two-hybrid  
 CC system. Also included are (1) a recombinant host cell expressing the  
 CC interactions between the Shigella flexneri polypeptide and a mammalian  
 CC polypeptide defined in the specification; (2) selecting a modulating

CC compound that inhibits or activates the protein-protein interactions; (3)  
 CC a modulating compound obtained from the method of (2); (4) a SID  
 CC (selected interacting domain) polypeptide or its fragment or variant  
 CC comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a  
 CC SID polynucleotide or its fragment or variant comprising encoding the  
 CC above polypeptides a vector comprising (5); (6) a recombinant host cell  
 CC containing the vector; and (10) a protein chip comprising Shigella  
 CC flexneri polypeptide and a mammalian polypeptide defined in the  
 CC specification. A pharmaceutical composition comprising the compound,  
 CC polypeptide or polynucleotide is useful for treating or preventing  
 CC shigellosis (bacillary dysentery) in a human or mammal. The present  
 CC sequence represents a human prey protein isolated by the yeast two-hybrid  
 CC assay, forming a complex of the invention with a shigella protein  
 XX  
 SX Sequence 158 AA;

Query Match 100.0%; Score 582; DB 5; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AHKPSLTDTPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQLNGRCCLREAQYSML 60  
 DB 48 AHKPSLTDTPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQLNGRCCLREAQYSML 107  
 QY 61 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 111  
 DB 108 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 158

RESULT 3  
 ABW00828  
 ID ABW00828 standard; protein; 426 AA.  
 XX  
 AC ABW00828;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human p55-R protein.  
 XX  
 KW Intracellular domain; IC; p55 tumour necrotic factor receptor; TNF;  
 KW tumour; rheumatoid arthritis; inflammatory disease; gene therapy;  
 KW cytostatic; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 206..426  
 FT Domain /note="p55 intracellular domain (IC)"  
 FT Domain 328..426  
 FT Domain /note="Death domain"

US6579697-B1  
 17-JUN-2003.

XX PF 12-NOV-1996; 96US-00747562.  
 XX  
 XX PR 11-MAY-1995; 95WO-US0005854.  
 XX  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 XX Wallach D, Boldin M, Mett I, Varfolomeev E;  
 XX WPI; 2003-799831/75.  
 XX  
 PT New DNA molecule encoding a polypeptide capable of binding to an  
 PT intracellular domain of a p55 tumor necrotic factor (TNF) receptor,  
 PT useful for preparing a composition for treating tumor, rheumatoid  
 PT arthritis or inflammatory diseases.  
 XX  
 PS Claim 1; Col 101-104; 126pp; English.  
 XX  
 CC The invention relates to an isolated DNA molecule which encodes a

CC polypeptide capable of binding to an intracellular domain of a p55 tumour  
 CC necrotic factor (TNF) receptor. The DNA molecule is useful for preparing  
 CC a composition for treating tumour, rheumatoid arthritis or inflammatory  
 CC diseases. The invention is useful in gene therapy. The present sequence  
 CC is the human p55C-R protein

XX  
 SQ Sequence 426 AA;  
 Query Match 100.0%; Score 582; DB 7; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AHKPSLDTDDPATLYAVVENPPPLRWKFVRRRLGSLDHEIDRLQLNGRCLREAYSM 60  
 Db 316 AHKPSLDTDDPATLYAVVENPPPLRWKFVRRRLGSLDHEIDRLQLNGRCLREAYSM 375  
 QY 61 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
 Db 376 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 426

## RESULT 4

AAB50895

ID AAB50895 standard; protein; 453 AA.

XX

AC AAB50895;

XX

DT 19-MAR-2001 (first entry)

XX

DE Human TNFR 1.

XX

KW Human; TR10 receptor; cytostatic; immunosuppressive; neuroprotective;  
 KW antiinflammatory; anti-HIV; antiparkinsonian; nootropic; cardiant;  
 KW vasotrophic; antiallergic; antidiabetic; vulnaray; ophthalmological;  
 KW antiviral; antibacterial; antifungal; antiparasitic; Gene therapy; TNFR;  
 KW tumour necrosis factor receptor; cancer; leukaemia; autoimmune disorder;  
 KW apoptosis; cardiovascular disorder; inflammatory disease; wound;  
 KW infection; neurological disease; protein coordinate data.

XX

OS Homo sapiens.

XX

PN WO200073321-A1.

XX

PD 07-DEC-2000.

XX

PF 26-MAY-2000; 2000WO-US014554.

XX

PR 28-MAY-1999; 99US-0136786P.

XX

PR 07-JUL-1999; 99US-0142563P.

XX

PR 15-JUL-1999; 99US-0144023P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ni J;

XX

XX WPI; 2001-025250/03.

XX

PT Nucleic acid encoding a tumor necrosis factor receptor 10, useful in the  
 PT diagnosis, treatment or prevention of cancer, autoimmune disorders, and  
 PT diseases and disorders associated with apoptosis.

XX

PS Disclosure; Fig 2; 212pp; English.

XX

CC The present sequence is given in a specification relating to an isolated  
 CC nucleic acid encoding a human tumour necrosis factor receptor TR10. The  
 CC TR10 polynucleotide, polypeptide, antibodies, agonists and antagonists  
 CC are useful in the diagnosis, treatment or prevention of cancer, such as  
 CC breast and ovarian cancer and leukaemia; autoimmune disorders such as  
 CC multiple sclerosis, Crohn's disease and graft versus host disease;  
 CC diseases associated with increased apoptosis such as AIDS, Alzheimer's  
 CC disease and Parkinson's disease; cardiovascular disorders such as limb  
 CC ischaemia and congenital heart defects; inflammatory diseases e.g.  
 CC allergy; wound healing; disorders associated with neovascularisation,

XX

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XX

XX

XX

CC e.g. diabetic retinopathy; infectious diseases such as viral, bacterial,  
 CC fungal and parasitic infections; and neurological diseases such as  
 CC amyotrophic lateral sclerosis

XX  
 SQ Sequence 453 AA;  
 Query Match 100.0%; Score 582; DB 4; Length 453;  
 Best Local Similarity 100.0%; Pred. No. 9e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AHKPSLDTDDPATLYAVVENPPPLRWKFVRRRLGSLDHEIDRLQLNGRCLREAYSM 60  
 Db 343 AHKPSLDTDDPATLYAVVENPPPLRWKFVRRRLGSLDHEIDRLQLNGRCLREAYSM 402  
 QY 61 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
 Db 403 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 453

## RESULT 5

ABG74755

ID ABG74755 standard; protein; 455 AA.

XX

AC ABG74755;

XX

DT 14-MAY-2003 (first entry)

XX

DE Human TNF-R protein huTNF-R.

XX

KW TNF; human; tumour necrosis factor; tumour necrosis factor receptor;  
 KW TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.

XX

OS Homo sapiens.

XX

PN EP393438-A.

XX

PD 24-OCT-1990.

XX

PF 06-APR-1990; 90EP-00106624.

XX

PR 21-APR-1989; 89DE-03913101.

XX

PR 21-JUN-1989; 89DE-03920282.

XX

PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.

XX

PA (SYND) SYNERGEN INC.

XX

PI Hauptmann R, Himmeler A, Maurerfoggy I, Stratowa C;

XX

XX WPI; 1990-321987/43.

XX

XX N-PSDB; ABQ77487.

XX

PT DNA encoding TNF binding protein and TNF- receptor - used in tumour  
 PT treatment and to understand mechanisms to TNF action.

XX

PS Example 9; Fig 9; 51pp; German.

XX

CC This invention describes novel polynucleotide sequences encoding tumour  
 CC necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).  
 CC The products of the invention are useful in pharmaceutical compositions  
 CC for prophylaxis or treatment of human tumours and to understand the  
 CC mechanisms of TNF action. This sequence represents the huma TNF-R, huTNF-  
 CC R described in the disclosure of the invention

XX

SQ Sequence 455 AA;

XX

Query Match 100.0%; Score 582; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 9e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX

XX

XX

QY 1 AHKPSLDTDDPATLYAVVENPPPLRWKFVRRRLGSLDHEIDRLQLNGRCLREAYSM 60  
 Db 345 AHKPSLDTDDPATLYAVVENPPPLRWKFVRRRLGSLDHEIDRLQLNGRCLREAYSM 404

QY 61 ATWRRTPREATLEILGRVLRDMLGCLDEIEALCGPALPPAPSLR 111  
 XX |||||  
 Db 405 ATWRRTPREATLEILGRVLRDMLGCLDEIEALCGPALPPAPSLR 455

## RESULT 6

AAR07451  
 ID AAR07451 standard; protein; 455 AA.  
 XX AAR07451;  
 AC AAR07451;  
 DT 25-MAR-2003 (revised)  
 DT 29-JAN-1991 (first entry)  
 XX Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.  
 DE  
 XX Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;  
 KW infectious disease; parasitic disease; cachexia; autoimmune disease;  
 KW shock; lambdaTNF-R2; raTNF-R8.  
 XX  
 XX Homo sapiens.  
 OS  
 XX EP393438-A.  
 PN  
 XX 24-OCT-1990.  
 PD  
 XX 06-APR-1990; 90EP-00106624.  
 PF  
 XX 21-APR-1989; 89DE-03913101.  
 PR  
 XX 21-JUN-1989; 89DE-03920282.  
 PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 PA (SYND ) SYNERGEN INC.  
 XX  
 XX Hauptmann R, Himmler A, Maurerfogy I, Stratowa C;  
 PI  
 XX WPI; 1990-321987/43.  
 DR  
 XX N-PSDB; AAQ06285.  
 XX  
 XX DNA encoding TNF binding protein and TNF- receptor - used in tumour  
 PT treatment and to understand mechanisms to TNF action.  
 PT  
 XX Disclosure; Fig 91(1-2); 5lpp; German.

CC raTNF-R8 (AAQ06284) was used to screen the HS913T cDNA library. LambdaTNF  
 CC -R2 encodes the complete human TNF-R2 and was used to construct a plasmid  
 CC (pADTNF-R) expressing the product the same way as pADTNF-BP (see  
 CC AAQ06282). The expressed proteins are useful prophylactically and  
 CC therapeutically to control disorders which involve the damaging effects  
 CC of TNF-alpha or -beta (e.g. infectious or parasitic diseases, shock,  
 CC cachexia, autoimmune diseases, adult respiratory distress syndrome etc.,  
 CC or side effects of treatment with TNF-alpha). They can also be used as  
 CC diagnostic reagents for assaying TNF and in study of TNF-receptor  
 CC interactions. See also AAQ06282-Q06285. (Updated on 25-MAR-2003 to  
 CC correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 455 AA;

Query Match 100.0%; Score 582; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 9e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSQSLDTPATLYAVVENVPLRWKEFVRLGSLDHEIDRLQNGRCLEAQYSML 60  
 |||||  
 Db 345 AHKPSQSLDTPATLYAVVENVPLRWKEFVRLGSLDHEIDRLQNGRCLEAQYSML 404

QY 61 ATWRRTPREATLEILGRVLRDMLGCLDEIEALCGPALPPAPSLR 111  
 XX |||||  
 Db 405 ATWRRTPREATLEILGRVLRDMLGCLDEIEALCGPALPPAPSLR 455

## RESULT 7

ABG74751

ID ABG74751 standard; protein; 455 AA.  
 XX ABG74751;  
 AC ABG74751;  
 DT 14-MAY-2003 (first entry)  
 XX Human TNF receptor protein.  
 DE  
 XX TNF; human; tumour necrosis factor; tumour necrosis factor receptor;  
 KW TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.  
 XX  
 XX Homo sapiens.  
 OS  
 XX EP393438-A.  
 PN  
 XX 24-OCT-1990.  
 PD  
 XX 06-APR-1990; 90EP-00106624.  
 PF  
 XX 21-APR-1989; 89DE-03913101.  
 PR  
 XX 21-JUN-1989; 89DE-03920282.  
 PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 PA (SYND ) SYNERGEN INC.  
 XX  
 XX Hauptmann R, Himmler A, Maurerfogy I, Stratowa C;  
 PI  
 XX WPI; 1990-321987/43.  
 DR  
 XX DNA encoding TNF binding protein and TNF- receptor - used in tumour  
 PT treatment and to understand mechanisms to TNF action.  
 PT  
 XX Claim 22; Page 34; 5lpp; German.

Query Match 100.0%; Score 582; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 9e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AHKPSQSLDTPATLYAVVENVPLRWKEFVRLGSLDHEIDRLQNGRCLEAQYSML 60  
 |||||  
 Db 345 AHKPSQSLDTPATLYAVVENVPLRWKEFVRLGSLDHEIDRLQNGRCLEAQYSML 404

QY 61 ATWRRTPREATLEILGRVLRDMLGCLDEIEALCGPALPPAPSLR 111  
 XX |||||  
 Db 405 ATWRRTPREATLEILGRVLRDMLGCLDEIEALCGPALPPAPSLR 455

## RESULT 8

AAR12550  
 ID AAR12550 standard; protein; 455 AA.

XX AAR12550;  
 AC AAR12550;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 12-SEP-1991 (first entry)  
 XX  
 DE Type I TNF receptor.  
 XX  
 XX Tumour Necrosis Factor; TNF; binding protein; TBP-I.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..21  
 FT

FT Domain /label= sig\_peptide  
 FT 21..203  
 FT /label= soluble domain  
 FT /note= "may be 2 amino acids shorter or contain a few  
 FT additional amino acids"  
 FT 22..455  
 FT Protein /label= mat\_protein  
 FT 41..53  
 FT Region /label= TBP-I derived sequence  
 FT 44..83  
 FT Region /label= repeat\_1  
 FT 54..56  
 FT Modified-site /label= N-glycosylation\_site  
 FT 84..126  
 FT Region /label= repeat\_2  
 FT 110..124  
 FT Region /label= TBP-I derived sequence  
 FT 127..167  
 FT Region /label= repeat\_3  
 FT 145..147  
 FT Modified-site /label= N-glycosylation\_site  
 FT 151..153  
 FT Modified-site /label= N-glycosylation\_site  
 FT 168..201  
 FT Region /label= repeat\_4  
 FT 199..201  
 FT Region /label= TBP-I derived sequence  
 FT 212..234  
 FT Domain /label= transmembrane\_domain  
 XX  
 PN EP433900-A.  
 XX  
 XX 26-JUN-1991.  
 XX  
 XX 13-DEC-1990; 90EP-00124133.  
 XX  
 XX 13-DEC-1989; 89IL-00092697.  
 XX 12-JUL-1990; 90IL-00095064.  
 XX  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 XX (WALL/ ) WALLACH D.  
 XX  
 XX Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;  
 PI Aderka D;  
 XX  
 XX WPI: 1991-186774/26.  
 DR N-PSDB; AAQ12215.  
 DR  
 XX Recombinant tumour necrosis factor binding protein I - prepd. by  
 PT transfecting eukaryotic cells with vector contg. deoxyribonucleic acid  
 PT encoding human type I TNF receptor or soluble domain.  
 PT  
 XX Disclosure; Fig 1(D); 30pp; English.  
 XX  
 CC The Tumour Necrosis Factor Binding Protein I is the soluble form of type  
 CC I TNF-receptor and constitutes a fragment of the cell surface form of  
 CC this receptor, corresp. to its extracellular domain. The soluble proteins  
 CC produced by the transfected cells secreted into the medium may have at  
 CC the N-terminus the sequence Asp-Ser-Val (41-43), or the sequence Leu-Val-  
 CC Pro (30-32) or Ile-Tyr-Pro (22-24) or any other sequence between Ile (21)  
 CC and Asp (41). See also AAQ12212-15. (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 XX  
 XX Sequence 455 AA;  
 SQ  
 Query Match 100.0%; Score 582; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 9e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 AHKPSQSLDTPATLYAVVNPPLRWKEFVRRLGSLDHEIDRLQNGRCLREAQYSML 60  
 345 AHKPSQSLDTPATLYAVVNPPLRWKEFVRRLGSLDHEIDRLQNGRCLREAQYSML 404

QY 61 ATWRRTPRRATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
 DB 405 ATWRRTPRRATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455  
 RESULT 9  
 AAR10986  
 ID AAR10986 standard; protein; 455 AA.  
 XX  
 AC AAR10986;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 13-MAY-1991 (first entry)  
 XX  
 DE 30kD TNF inhibitor precursor.  
 XX  
 KW Tumour necrosis factor; inhibitor.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Cleavage-site 40..41 /note= " cleavage gives active protein "  
 XX  
 PN AU9058976-A.  
 XX  
 PD 24-JAN-1991.  
 XX  
 PF 16-JUL-1990; 90AU-00058976.  
 XX  
 PR 18-JUL-1989; 89US-00381080.  
 PR 11-DEC-1989; 89US-00450329.  
 PR 07-FEB-1990; 90US-00479661.  
 XX  
 XX (SYND ) SYNERGEN INC.  
 XX  
 DR WPI: 1991-073847/11.  
 DR N-PSDB; AAQ10883.  
 XX  
 PT Tumour necrosis factor inhibitor - for suppression of tnf-alpha and -  
 FT beta, useful as therapeutic agent.  
 XX  
 PS Disclosure; Fig 21; 142pp; English.  
 XX  
 CC The sequence comprises the entire 30 kD TNF inhibitor. The clone from  
 CC which the sequence was deduced was isolated from a cDNA library prepd.  
 CC from RNA form U937 cells treated with PMA/PHA. The whole gene can be  
 CC inserted into expression vectors for prepn. of TNF inhibitor for use in  
 CC the treatment of inflammatory and degenerative diseases. The active  
 CC protein is claimed (claim 8). See also AAR10984 and AAR11001. (Updated on  
 CC 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 455 AA;  
 Query Match 100.0%; Score 582; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 9e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 AHKPSQSLDTPATLYAVVNPPLRWKEFVRRLGSLDHEIDRLQNGRCLREAQYSML 60  
 345 AHKPSQSLDTPATLYAVVNPPLRWKEFVRRLGSLDHEIDRLQNGRCLREAQYSML 404  
 QY 61 ATWRRTPRRATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
 DB 405 ATWRRTPRRATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455  
 RESULT 10  
 AAR11082  
 ID AAR11082 standard; protein; 455 AA.  
 XX  
 AC AAR11082;  
 XX

DT 09-JAN-2003 (revised)  
 XX 24-MAY-1991 (first entry)  
 DE Human 55kD TNF-binding protein.  
 XX  
 XX Tumour Necrosis Factor; binding proteins; septic shock;  
 KW autoimmune glomerulonephritis; lymphokine; cytokine.  
 XX  
 XX Homo sapiens.

Key Location/Qualifiers  
 FT Peptide 1..28  
 FT Modified-site /label= signal peptide  
 FT Modified-site 54  
 FT Modified-site /label= putative N-glycosylation site  
 FT Modified-site 145  
 FT Modified-site /label= putative N-glycosylation site  
 FT Modified-site 151  
 FT Region /label= putative N-glycosylation site  
 FT 212..230  
 FT /label= transmembrane region  
 FT Modified-site 270  
 FT /label= putative N-glycosylation site

XX EP417563-A.

XX 20-MAR-1991.

XX 31-AUG-1990; 90EP-00116707.

XX 12-SEP-1989; 89CH-00003319.

PR 08-MAR-1990; 90CH-00000746.

PR 20-APR-1990; 90CH-00001347.

XX (HOFF) HOFFMANN-IA ROCHE AG.

XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;

PI Schlaeger EJ;

DR WPI: 1991-081851/12.

DR N-PSDB; AAQ10955.

XX Insoluble tumour necrosis factor binding proteins - and DNA encoding  
 FT them, useful in pharmaceutical prods. and for antibody prodn.

XX Claim 1; Fig 1; 26pp; German.

XX Partial amino acid sequences were determined for the 55 and 75kD TNF-BPs  
 CC (see AAR1072-R11081) and oligonucleotide primers were synthesised based  
 CC on these partial sequences. The primers were used to produce a cDNA  
 CC fragment for use as a probe to screen a human placental cDNA bank  
 CC constructed in lambda gt11. Positive clones were identified and sequenced.  
 CC DNA constructs comprising the TNF-BP coding sequence may also contain a  
 CC fragment encoding a human Ig domain. Recombinant constructs are used to  
 CC transform cells to confer improved TNF-binding properties. See also  
 CC AAQ10956. (Updated on 09-JAN-2003 to add missing OS field.)

XX Sequence 455 AA;

Query Match 100.0%; Score 582; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 9e-61;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRIGLSDEHIDRLQLONGRCLEAQYSML 60

DB 345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRIGLSDEHIDRLQLONGRCLEAQYSML 404

QY 61 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 111

DB 405 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 11

AAR20787

ID AAR20787 standard; protein; 455 AA.

XX

AC AAR20787;

XX

DT 11-MAY-1992 (first entry)

XX

DE TNF-alpha binding protein.

XX

KW Tumour necrosis factor alpha; autoimmune diseases; cachectin;

KW extracellular domain.

XX

OS Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..40

FT Domain /note= "signal peptide"

FT Peptide 30..199

FT /note= "extracellular domain"

FT Peptide 41..455

FT /note= "mature peptide"

FT Modified-site 145..147

FT /note= "potential N-glycosylation site"

FT Modified-site 151..153

FT /note= "potential N-glycosylation site"

FT Domain 212..234

FT /note= "transmembrane domain"

XX

PN GB2246569-A.

XX

PD 05-FEB-1992.

XX

PF 15-JUN-1990; 90GB-00013410.

XX

PR 15-JUN-1990; 90GB-00013410.

XX

PA (CHAR-) CHARING CROSS SUNLE.

PI

PI Feldman M, Gray P, Turner M, Brennan F;

XX

XX WPI: 1992-043613/06.

DR N-PSDB; AAQ20973.

XX

PT New tumour necrosis factor alpha binding protein and polypeptide - useful  
 PT in treating cachexia, sepsis and autoimmune diseases e.g. rheumatoid  
 PT arthritis.

XX

PS Disclosure; Fig 1; 25pp; English.

XX

CC The amino acid sequence is that of tumour necrosis factor alpha binding  
 CC protein which contains the extracellular domain of human TNF alpha  
 CC receptor. It is soluble and can be used in the regulation of TNF-mediated  
 CC responses by binding and sequestering the cytokine. It can therefore be  
 CC used therapeutically to treat disorders such as cachexia, sepsis and  
 CC autoimmune diseases, specifically rheumatoid arthritis

XX Sequence 455 AA;

Query Match 100.0%; Score 582; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 9e-61;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRIGLSDEHIDRLQLONGRCLEAQYSML 60

DB 345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRIGLSDEHIDRLQLONGRCLEAQYSML 404

QY 61 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 111

DB 405 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 12

AAR42059



ID AAR42059 standard; protein; 455 AA.  
 AC AAR42059;  
 XX  
 XX 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 29-APR-1994 (first entry)  
 XX  
 XX Lambda derived TNF-R.  
 DE  
 XX  
 XX Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;  
 KW IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;  
 KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;  
 KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;  
 KW graft versus host disease; sepsis; inflammation; allergy;  
 KW autoimmune dysfunction.  
 XX  
 XX Homo sapiens.  
 OS Bacteriophage lambda.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 1..40  
 FT /note= "Signal peptide"  
 FT Protein 41..455  
 FT /note= "Mature hTNF-R"  
 XX  
 XX WO9319777-A1.  
 XX  
 XX 14-OCT-1993.  
 PD  
 XX 26-MAR-1993; 93WO-US002938.  
 XX  
 XX 30-MAR-1992; 92US-00860710.  
 XX  
 XX (IMMV ) IMMUNEX CORP.  
 PA  
 XX Smith CA;  
 PI  
 XX WPI; 1993-336592/42.  
 DR N-PSDB; AAQ49932.  
 XX  
 XX New fusion protein tumour necrosis factor and human interleukin-1  
 PT receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid  
 PT arthritis, diabetes, cerebral malaria, sepsis, etc.  
 XX  
 XX Disclosure; Page 57-59; 85pp; English.  
 PS  
 XX The sequences given in AAR42058-59 represent human tumour necrosis  
 CC factor receptor (TNF-R) and the sequences in AAR42060-61 represent human  
 CC interleukin-1 receptor (IL-1R). These sequences were used in the  
 CC production of a fusion protein which conformed to one of the formulae:  
 CC TNF-R-linker-TNF-R-linker-IL-1R IL-1R-linker-TNF-R-linker-TNF-R or TNF-R-  
 CC linker-TNF-R The linker may comprise 5-100 amino acids selected from Gly,  
 CC Asp, Ser, Thr and Ala. These linkers separate the individual moieties by  
 CC such a distance that each component of the fusion protein is capable of  
 CC folding into the secondary or tertiary structure required for its  
 CC biological activity. These fusion proteins may be used in therapy,  
 CC diagnosis and assays for conditions mediated by TNF or IL-1, particularly  
 CC in conditions in which both TNF and IL-1 play a causative role. They may  
 CC be used to treat cachexia, rheumatoid arthritis, diabetes, multiple  
 CC sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft  
 CC and xenograft rejection in graft versus host disease, sepsis, septic  
 CC shock, inflammation, allergies and autoimmune dysfunctions. (Updated on  
 CC 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS  
 CC field.)  
 XX  
 XX Sequence 455 AA;  
 SQ  
 Query Match 100.0%; Score 582; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 9e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AHKPSQSLDTPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQNGRCLEAQAQYML 60

DB 345 AHKPSQSLDTPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQNGRCLEAQAQYML 404  
 QY 61 ATWRRTPPREATLELLGHVLRMDLLGCLDEEALCGPALPPAPSLR 111  
 DB 405 ATWRRTPPREATLELLGHVLRMDLLGCLDEEALCGPALPPAPSLR 455  
 XX  
 XX RESULT 13  
 XX AAR51034  
 ID AAR51034 standard; protein; 455 AA.  
 AC AAR51034;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 13-MAY-1994 (first entry)  
 XX  
 XX Mutant p55 tumour necrosis factor receptor.  
 DE  
 XX  
 XX TNF; tumour necrosis factor; receptor; disease; autoimmunity;  
 KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;  
 KW effector protein.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FT Region 1..21  
 FT /label= Leader peptide.  
 FT Domain 183..205  
 FT /label= Transmembrane domain.  
 XX  
 XX EP568925-A2.  
 XX  
 XX 10-NOV-1993.  
 PD  
 XX 29-APR-1993; 93EP-00106981.  
 XX  
 XX 03-MAY-1992; 92IL-00101769.  
 XX  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 PA  
 XX Wallach D, Brakebusch C;  
 PI  
 XX WPI; 1993-353057/45.  
 DR N-PSDB; AAQ50870.  
 XX  
 XX Modulating activity of tumour necrosis factor receptor - using  
 PT peptide(s), antibodies, etc. which interact with critical regions of  
 PT receptor or effector protein, for controlling auto-immune disease, septic  
 PT shock, etc.  
 XX  
 XX Claim 5; Fig 1; 17pp; English.  
 PS  
 XX Modification of the tumour necrosis factor receptor by mutation or  
 CC deletion modulates signal transduction and/or cleavage effected by the  
 CC receptor. This modulation of activity can also be achieved using effector  
 CC proteins which interact with the TNF receptor. Molecules which interact  
 CC with the TNF receptor or the effector proteins can be used to treat or  
 CC prevent diseases associated with TNF activity e.g. autoimmune disease;  
 CC rheumatoid arthritis; graft rejection; graft vs. host disease or septic  
 CC shock. They can also be used to treat overdoses of exogenous TNF.  
 CC Specific deletions include amino acid residues 405-426 from which it was  
 CC discovered that amino acids 405-414, or part of them, are essential for  
 CC the signalling of the human p55 TNF-R for the cytotoxic effect of TNF  
 CC whereas amino acids 415-426 are not essential. Also residues 170-174, 174  
 CC -179 or both i.e 170-179 were deleted. This region of amino acids, or  
 CC part of, when deleted, abolished shedding of the soluble extracellular  
 CC forms of the protein. This sequence corresponds to the wild type protein  
 CC disclosed in AAR42197 except that alanine at position 197 has been  
 CC substituted in place of serine. The substitution inhibits cleavage of the  
 CC soluble form of the protein. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX

SQ Sequence 455 AA;  
 Query Match 100.0%; Score 582; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 9e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSQIDTDDPATLYAVVENVPPPLRWKFEVRLGLSDHEIDRLQLONGRCLEAQSML 60  
 DB 345 AHKPSQIDTDDPATLYAVVENVPPPLRWKFEVRLGLSDHEIDRLQLONGRCLEAQSML 404

QY 61 ATWRRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
 DB 405 ATWRRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 14  
 AAR42197  
 ID AAR42197 standard; protein; 455 AA.  
 XX AAR42197;  
 AC AAR42197;  
 XX 25-MAR-2003 (revised)  
 DT 13-MAY-1994 (first entry)  
 XX  
 DE p55 Tumour necrosis factor receptor.  
 XX  
 XX TNF; tumour necrosis factor; receptor; disease; autoimmunity;  
 KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;  
 KW effector protein.  
 XX  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..21  
 FT /label= Leader peptide.  
 FT Domain 183..205  
 FT /label= Transmembrane domain.  
 FT  
 XX EF569925-A2.  
 XX  
 PD 10-NOV-1993.  
 XX  
 PF 29-APR-1993; 93EP-00106981.  
 XX  
 PR 03-MAY-1992; 92IL-00101769.  
 XX  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 XX Wallach D, Brakebusch C;  
 XX  
 XX WPI; 1993-353057/45.  
 DR N-PSDB; AAQ50870.  
 DR  
 XX Modulating activity of tumour necrosis factor receptor - using  
 PT peptide(s), antibodies, etc. which interact with critical regions of  
 PT receptor or effector protein, for controlling auto-immune disease, septic  
 PT shock, etc.  
 XX  
 PS Claim 2; Fig 1; 17pp; English.  
 XX  
 XX Modification of the tumour necrosis factor receptor by mutation or  
 CC deletion modulates signal transduction and/or cleavage effected by the  
 CC receptor. This modulation of activity can also be achieved using effector  
 CC proteins which interact with the TNF receptor. Molecules which interact  
 CC with the TNF receptor or the effector proteins can be used to treat or  
 CC prevent diseases associated with TNF activity e.g. autoimmune disease;  
 CC rheumatoid arthritis; graft rejection; graft vs. host disease or septic  
 CC shock. They can also be used to treat overdoses of exogenous TNF.  
 CC Specific deletions include amino acid residues 405-426 from which it was  
 CC discovered that amino acids 405-414, or part of them, are essential for  
 CC the signalling of the human p55 TNF-R for the cytotoxic effect of TNF  
 CC whereas amino acids 415-426 are not essential. Also residues 170-174, 174  
 CC -179 or both i.e 170-179 were deleted. This region of amino acids, or

CC part of, when deleted, abolished shedding of the soluble extracellular  
 CC forms of the protein. (Updated on 25-MAR-2003 to correct PN field.)

XX  
 SQ Sequence 455 AA;  
 Query Match 100.0%; Score 582; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 9e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSQIDTDDPATLYAVVENVPPPLRWKFEVRLGLSDHEIDRLQLONGRCLEAQSML 60  
 DB 345 AHKPSQIDTDDPATLYAVVENVPPPLRWKFEVRLGLSDHEIDRLQLONGRCLEAQSML 404

QY 61 ATWRRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
 DB 405 ATWRRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 15  
 AAR75084  
 ID AAR75084 standard; protein; 455 AA.  
 XX AAR75084;  
 AC AAR75084;  
 XX 19-JAN-1996 (first entry)  
 DT  
 XX  
 DE p55 TNF-R.  
 XX  
 XX p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;  
 KW epidermal growth factor receptor; EGF-R; protease; inhibitor;  
 KW phorbol myristate acetate; PMA.  
 XX  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 41..53  
 FT /note= "N terminus of soluble p55 TNF-R"  
 FT Modified-site 54..56  
 FT /note= "glycosylation site"  
 FT Modified-site 145..147  
 FT /note= "glycosylation site"  
 FT Modified-site 161..163  
 FT /note= "glycosylation site"  
 FT Peptide 193..210  
 FT /note= "peptide used in creation of chimeras"  
 FT Region 198..210  
 FT /note= "spacer region"  
 FT Misc-difference 201  
 FT /note= "major C terminus for soluble p55 TNF-R"  
 FT Misc-difference 202  
 FT /note= "essential for shedding reaction"  
 FT Misc-difference 203  
 FT /note= "minor C terminus for soluble p55 TNF-R"  
 FT Region 212..234  
 FT /note= "transmembrane region"  
 XX  
 XX AU9475742-A.  
 XX  
 XX 04-MAY-1995.  
 XX  
 XX 11-OCT-1994; 94AU-00075742.  
 XX  
 XX 12-OCT-1993; 93IL-00107268.  
 XX  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 XX Wallach D, Brakebusch C, Varfolomeev E, Batkin M;  
 XX WPI; 1995-194342/26.  
 DR N-PSDB; AAQ90513.  
 XX  
 XX New protease capable of cleaving soluble tumour necrosis factor (TNF)  
 PT receptor - from cell-bound TNF- receptor, useful for antagonising

PT deleterious effects of TNF.  
XX  
PS  
PS Disclosure; Fig 1; 40pp; English.  
XX  
CC This sequence represents human p55 tumour necrosis factor (TNF-R).  
CC Expression of this receptor is regulated by shedding of the extracellular  
CC receptor fragment. The p55 TNF-R can be shed in response to different  
CC inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell  
CC type. The only region of the receptor whose structure affects the  
CC shedding response is the spacer region (see AAR75012) in the  
CC extracellular domain. This region is located close to a site of cleavage  
CC of the molecule, and links the Cys rich module to the transmembrane  
CC domain. The spacer region of the encoded protein was used to create the  
CC chimeras between human p55 TNF-R and murine epidermal growth factor  
CC receptor (EGF-R) that are represented by AAR75007-11. This spacer region  
CC was subjected to deletion mutations (AAR75013-25) and substitutions  
CC (AAR75026-47). Of the spacer region, the most important residues are Asn  
CC 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most important  
CC of these. The shedding of the receptor is independent of the side chain  
CC identity of these residues, with the exception of a limited dependence on  
CC the identity of Val 173. Mutations which alter the conformation of the  
CC protein adversely effect the shedding process. The mutations shown in  
CC AAR75013-47 were introduced in order to create an inhibitor of a protease  
CC that is capable of cleaving the soluble TNF-R from the cell bound TNF-R.  
CC Fragments of these inhibitors can be seen in AAR75017-9, AAR75025,  
CC AAR75033-5 and AAR75042-3. These protease inhibitors can be used for  
CC enhancing TNF function  
XX  
SQ Sequence 455 AA;  
  
Query Match 100.0%; Score 582; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 9e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLQLONGRCLREQYSML 60  
Db |||||  
345 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLQLONGRCLREQYSML 404  
  
QY 61 ATWRRTPREATLELGRVLRDMDLGGCLEDIEALCGPAALPPAPSLLR 111  
Db |||||  
405 ATWRRTPREATLELGRVLRDMDLGGCLEDIEALCGPAALPPAPSLLR 455

Search completed: June 1, 2004, 14:43:52  
Job time : 48.521 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:41:22 ; Search time 13.9581 Seconds  
(without alignments)  
410.549 Million cell updates/sec

Title: US-09-854-906-8

Perfect score: 582

Sequence: 1 AHKPSLDDPDLAYVVE.....DIEEALCGPALPPAPSLIR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/prodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/prodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/prodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582	100.0	426	4	US-08-747-562-37
2	582	100.0	453	3	US-09-086-483A-5
3	582	100.0	453	4	US-09-580-212-5
4	582	100.0	453	4	US-09-769-402-5
5	582	100.0	455	1	US-08-321-668-2
6	582	100.0	455	1	US-08-937-941-2
7	582	100.0	455	2	US-08-126-016-2
8	582	100.0	455	3	US-08-815-469-5
9	582	100.0	455	3	US-09-006-353A-3
10	582	100.0	455	4	US-09-527-236A-5
11	582	100.0	455	4	US-08-054-970-2
12	582	100.0	455	4	US-09-565-918-4
13	582	100.0	455	4	US-09-573-986-3
14	582	100.0	455	4	US-09-027-287-3
15	582	100.0	455	4	US-09-252-656B-3
16	582	100.0	455	4	US-08-406-824A-4
17	582	100.0	455	4	US-09-523-323-3
18	582	100.0	455	4	US-09-756-854-5
19	582	100.0	909	4	US-09-013-895A-4
20	582	100.0	909	4	US-09-448-868-4
21	577	99.1	455	1	US-08-050-319B-25
22	577	99.1	455	2	US-08-465-982-25
23	446	76.6	86	3	US-09-042-785A-25
24	446	76.6	108	2	US-08-580-988A-20
25	424	72.9	471	4	US-09-513-007-2
26	407	69.9	78	4	US-08-828-683A-23
27	397.5	68.3	84	4	US-09-069-827A-120

28	366	62.9	70	4	US-09-159-277A-6	Sequence 6, Appli
29	343.5	59.0	68	4	US-09-527-236A-23	Sequence 23, Appl
30	343.5	59.0	68	4	US-09-756-854-23	Sequence 23, Appl
31	329	56.5	64	4	US-08-894-626-3	Sequence 3, Appli
32	235	40.4	45	2	US-08-219-237B-11	Sequence 11, Appli
33	213	36.6	41	1	US-08-444-005-29	Sequence 29, Appl
34	192	33.0	41	1	US-08-444-005-23	Sequence 23, Appl
35	176	30.2	41	1	US-08-444-005-28	Sequence 28, Appl
36	168	28.9	833	4	US-09-013-895A-5	Sequence 5, Appli
37	168	28.9	833	4	US-09-448-868-5	Sequence 5, Appli
38	167.5	28.8	417	3	US-08-815-469-4	Sequence 4, Appli
39	167.5	28.8	417	3	US-09-153-927-2	Sequence 2, Appli
40	167.5	28.8	417	3	US-09-565-918-5	Sequence 5, Appli
41	167.5	28.8	417	4	US-08-928-069-10	Sequence 10, Appl
42	167.5	28.8	417	4	US-08-828-683A-6	Sequence 6, Appli
43	167.5	28.8	428	3	US-08-815-469-2	Sequence 2, Appli
44	166.5	28.6	35	1	US-08-444-005-35	Sequence 35, Appl
45	142	24.4	65	4	US-09-527-236A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-08-747-562-37  
; Sequence 37, Application US/08747562  
; Patent No. 6579697  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BOLDIN, Mark  
; APPLICANT: METT, Igor  
; APPLICANT: VARFOLOMBEV, Eugene  
; TITLE OF INVENTION: MODULATOR OF TNF/NGF SUPERFAMILY RECEPTORS  
; AND SOLUBLE OLIGOMERIC TNF/NGF SUPERFAMILY RECEPTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/747,562  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/05854  
; FILING DATE: 11-MAY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 109,632  
; FILING DATE: 11-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 111,125  
; FILING DATE: 02-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH=15A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 426 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-747-562-37

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Query Match      100.0%; Score 582; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e-62; Indels 0; Gaps 0;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENVPPPLRWKEFVRRGLSDHEIDRLQLONGRCCLREAYQSM 60
Db 316 AHKPSLDTDDPATLYAVVENVPPPLRWKEFVRRGLSDHEIDRLQLONGRCCLREAYQSM 375

QY 61 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 111
Db 376 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 426

RESULT 2
US-09-086-483A-5
; Sequence 5, Application US/09086483A
; Patent No. 6214580
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,483A
; FILING DATE: May-29-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,936
; FILING DATE: May-30-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/069,112
; FILING DATE: Dec-9-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-086-483A-5

Query Match      100.0%; Score 582; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.6e-62; Indels 0; Gaps 0;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENVPPPLRWKEFVRRGLSDHEIDRLQLONGRCCLREAYQSM 60
Db 343 AHKPSLDTDDPATLYAVVENVPPPLRWKEFVRRGLSDHEIDRLQLONGRCCLREAYQSM 402

QY 61 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 111
Db 403 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 453
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RESULT 3
US-09-580-212-5
; Sequence 5, Application US/09580212
; Patent No. 6506569
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR10
; FILE REFERENCE: PF379P1
; CURRENT APPLICATION NUMBER: US/09/580,212
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,786
; PRIOR FILING DATE: 1999-05-23
; PRIOR APPLICATION NUMBER: 60/142,563
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/144,023
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-580-212-5

Query Match      100.0%; Score 582; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.6e-62; Indels 0; Gaps 0;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENVPPPLRWKEFVRRGLSDHEIDRLQLONGRCCLREAYQSM 60
Db 343 AHKPSLDTDDPATLYAVVENVPPPLRWKEFVRRGLSDHEIDRLQLONGRCCLREAYQSM 402

QY 61 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 111
Db 403 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 453

RESULT 4
US-09-769-402-5
; Sequence 5, Application US/09769402
; Patent No. 6607726
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/769,402
; FILING DATE: 26-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/086,483
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 60/069,112
; FILING DATE: Dec-9-97
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF379
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: amino acid  
STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-769-402-5

Query Match 100.0%; Score 582; DB 4; Length 453;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDLTDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLQNGRCLREAOYSML 60  
DB 343 AHKPSLDLTDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLQNGRCLREAOYSML 402  
QY 61 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
DB 403 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 453

RESULT 5  
US-08-321-668-2  
Sequence 2, Application US/08321668  
Patent No. 566589  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKEBUSCH, Cord  
APPLICANT: VARFOLOMEV, Eugene  
APPLICANT: BATKIN, Michael  
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/321,668  
FILING DATE: 12-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 107268  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=13  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-321-668-2

Query Match 100.0%; Score 582; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDLTDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLQNGRCLREAOYSML 60  
DB 345 AHKPSLDLTDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLQNGRCLREAOYSML 404  
QY 61 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
DB 405 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 6  
US-08-837-941-2  
Sequence 2, Application US/08837941  
Patent No. 5766917  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKEBUSCH, Cord  
APPLICANT: VARFOLOMEV, Eugene  
APPLICANT: BATKIN, Michael  
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837,941  
FILING DATE: 28-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/321,668  
FILING DATE: 12-OCT-1994  
APPLICATION NUMBER: IL 107268  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=13  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-837-941-2

Query Match 100.0%; Score 582; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 345 AHKPSLDLTDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLQNGRCLREAOYSML 404  
QY 61 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
DB 405 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 7  
US-08-126-016-2  
; Sequence 2, Application US/08126016  
; Patent No. 5811261  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, DAVID  
; APPLICANT: NOPHAR, YARON  
; APPLICANT: KEMPER, OLIVER  
; APPLICANT: ENGELMANN, HARTMUT  
; APPLICANT: BRAKEBUSCH, CORD  
; APPLICANT: ADERKA, DAN  
; TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR  
; TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/126,016  
; FILING DATE: 24-SEP-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/625668  
; FILING DATE: 13-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, ROGER L  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
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; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
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RESULT 8  
US-08-815-469-5  
; Sequence 5, Application US/08815469  
; Patent No. 6153402  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
  
Query Match 100.0%; Score 582; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 61 ATWRRTPREATLELGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
Db 405 ATWRRTPREATLELGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/03/815,469  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 6153402 Yet Assigned  
; FILING DATE: 06-FEB-1997  
; APPLICATION NUMBER: US 60/028,711  
; FILING DATE: 17-OCT-1996  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 60/013,285  
; FILING DATE: 12-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
; US-08-815-469-5  
  
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Db 405 ATWRRTPREATLELGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455  
  
RESULT 9  
US-09-006-353A-3  
; Sequence 3, Application US/09006353A  
; Patent No. 6261801  
; GENERAL INFORMATION:  
; APPLICANT: WEI, YING-FEI  
; APPLICANT: YU, GUO-LIANG  
; APPLICANT: GENTZ, REINER  
; APPLICANT: RUBEN, STEVEN  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US

1 ; ZIP: 20850  
2 ; COMPUTER READABLE FORM:  
3 ; MEDIUM TYPE: Floppy disk  
4 ; COMPUTER: IBM PC compatible  
5 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
6 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
7 ; CURRENT APPLICATION DATA:  
8 ; APPLICATION NUMBER: US/09/006,353A  
9 ; FILING DATE:  
10 ; CLASSIFICATION: 435  
11 ; ATTORNEY/AGENT INFORMATION:  
12 ; NAME: BROOKES, ANDERS A  
13 ; REGISTRATION NUMBER: 36,373  
14 ; REFERENCE/DOCKET NUMBER: PF341  
15 ; TELECOMMUNICATION INFORMATION:  
16 ; TELEPHONE: (301) 309-8504  
17 ; TELEFAX: (301) 309-8512  
18 ; INFORMATION FOR SEQ ID NO: 3:  
19 ; SEQUENCE CHARACTERISTICS:  
20 ; LENGTH: 455 amino acids  
21 ; TYPE: amino acid  
22 ; STRANDEDNESS: single  
23 ; TOPOLOGY: linear  
24 ; MOLECULE TYPE: protein  
25 ; US-09-006-353A-3

Query Match 100.0%; Score 582; DB 3; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 61 ATWRRTPREATLLGLRVLRDMLLGLCLEDIEEALCGPAALPPAPSLR 111  
Db 405 ATWRRTPREATLLGLRVLRDMLLGLCLEDIEEALCGPAALPPAPSLR 455

RESULT 10  
US-09-527-236A-5  
; Sequence 5, Application US/09527236A  
; Patent No. 6358508  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Fan, Ping  
; APPLICANT: Gentz, Reiner L.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
; FILE REFERENCE: PF375P1  
; CURRENT APPLICATION NUMBER: US/09/527,236A  
; CURRENT FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/052,991  
; PRIOR FILING DATE: 1997-06-11  
; PRIOR APPLICATION NUMBER: 09/095,094  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/126,019  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: 60/134,220  
; PRIOR FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-527-236A-5

Query Match 100.0%; Score 582; DB 4; Length 455;  
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QY 61 ATWRRTPREATLLGLRVLRDMLLGLCLEDIEEALCGPAALPPAPSLR 111  
Db 405 ATWRRTPREATLLGLRVLRDMLLGLCLEDIEEALCGPAALPPAPSLR 455  
  
RESULT 11  
US-08-054-970-2  
; Sequence 2, Application US/08054970  
; Patent No. 6395267  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BRAKEBUSCH, Cord  
; TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/054,970  
; FILING DATE: 03-MAY-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: WALLACH=9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-054-970-2

Query Match 100.0%; Score 582; DB 4; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 61 ATWRRTPREATLLGLRVLRDMLLGLCLEDIEEALCGPAALPPAPSLR 111  
Db 405 ATWRRTPREATLLGLRVLRDMLLGLCLEDIEEALCGPAALPPAPSLR 455

RESULT 12  
US-09-565-918-4  
; Sequence 4, Application US/09565918  
; Patent No. 6433147  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Fan, James G.  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dixit, Vishva M.  
; TITLE OF INVENTION: Death Domain Containing Receptor 4



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; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/09/565,918
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-918-4

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Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 405 ATWRRTPREATLELGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 13
US-09-573-986-3
; Sequence 3, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-pei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-3

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Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
US-09-027-287-3
; Sequence 3, Application US/09027287A
; Patent No. 6479254
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
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; APPLICANT: Ruben, Steven M.
; APPLICANT: Ullrich, Stephen
; TITLE OF INVENTION: Apoptosis Inducing Molecule II
; FILE REFERENCE: 1488.0650004
; CURRENT APPLICATION NUMBER: US/09/027,287A
; CURRENT FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: US 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: US 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: US 60/030,157
; EARLIER FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: US 60/013,923
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-027-287-3

Query Match      100.0%; Score 582; DB 4; Length 455;
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Db 405 ATWRRTPREATLELGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 15
US-09-252-656B-3
; Sequence 3, Application US/09252656B
; Patent No. 6495520
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Zhang, Jun
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.0650006
; CURRENT APPLICATION NUMBER: US/09/252,656B
; CURRENT FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 60/075,409
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/027,287
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/003,886
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 08/822,953
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/013,923
; PRIOR FILING DATE: 1996-03-22
; PRIOR APPLICATION NUMBER: US 60/030,157
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 61
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; SEQ ID NO 3
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-252-656B-3

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Best Local Similarity 100.0%; Pred. No. 1.6e-62;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Title: US-09-854-906-8

Perfect score: 582

Sequence: 1 AHKPSQSDTDDPATLYAVVE.....DIEEALCGPAALPPAPSLLR 111

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	582	100.0	455	9	US-09-826-212-3
5	582	100.0	455	9	US-09-333-966-5
6	582	100.0	455	9	US-09-287-287-3
7	582	100.0	455	9	US-09-874-138-3
8	582	100.0	455	9	US-09-840-707A-16
9	582	100.0	455	9	US-09-252-656B-3
10	582	100.0	455	9	US-09-899-422-2
11	582	100.0	455	9	US-09-899-422-17
12	582	100.0	455	9	US-09-935-727-5
13	582	100.0	455	9	US-09-898-234-2
14	582	100.0	455	9	US-09-898-234-17
15	582	100.0	455	9	US-09-756-854-5

16	582	100.0	455	9	US-09-899-429A-2	Sequence 2, Appli
17	582	100.0	455	9	US-09-899-429A-27	Sequence 27, Appl
18	582	100.0	455	9	US-09-792-356-2	Sequence 2, Appli
19	582	100.0	455	9	US-09-792-356-17	Sequence 17, Appl
20	582	100.0	455	10	US-09-314-889-5	Sequence 5, Appli
21	582	100.0	455	10	US-09-945-505-3	Sequence 3, Appli
22	582	100.0	455	12	US-10-099-007A-13	Sequence 13, Appl
23	582	100.0	455	13	US-10-005-842-3	Sequence 3, Appli
24	582	100.0	455	13	US-10-120-397-2	Sequence 2, Appli
25	582	100.0	455	13	US-10-041-574-5	Sequence 5, Appli
26	582	100.0	455	14	US-10-252-408-4	Sequence 4, Appli
27	582	100.0	455	14	US-10-038-557A-16	Sequence 16, Appl
28	582	100.0	455	14	US-10-173-902-4	Sequence 4, Appli
29	582	100.0	455	14	US-10-186-643-3	Sequence 5, Appli
30	582	100.0	455	14	US-10-189-189-5	Sequence 3, Appli
31	582	100.0	455	15	US-10-375-680-3	Sequence 3, Appli
32	582	100.0	455	15	US-10-418-242-5	Sequence 5, Appli
33	582	100.0	455	15	US-10-440-464-59	Sequence 59, Appl
34	582	100.0	909	14	US-10-226-296-4	Sequence 4, Appli
35	582	100.0	909	14	US-10-226-318-4	Sequence 4, Appli
36	424	72.9	471	9	US-09-970-532-2	Sequence 2, Appli
37	407	69.9	78	9	US-09-887-879-16	Sequence 16, Appl
38	407	69.9	78	9	US-09-992-964-16	Sequence 10, Appl
39	407	69.9	78	12	US-10-207-295-10	Sequence 23, Appl
40	407	69.9	78	13	US-10-112-793-23	Sequence 15, Appl
41	407	69.9	78	14	US-10-242-383-16	Sequence 15, Appl
42	386	66.3	461	9	US-09-898-422-15	Sequence 25, Appl
43	386	66.3	461	9	US-09-898-234-15	Sequence 15, Appl
44	386	66.3	461	9	US-09-899-429A-25	Sequence 15, Appl
45	386	66.3	461	9	US-09-792-356-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1  
US-10-043-487-301  
; Sequence 301, Application US/10043487  
; Publication No. US20030055220A1  
; GENERAL INFORMATION:  
; APPLICANT: HYBRIGENICS  
; APPLICANT: Pierre, LEGRAIN  
; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptid  
; FILE REFERENCE: B4778A  
; CURRENT APPLICATION NUMBER: US/10/043,487  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/261,130  
; PRIOR FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 561  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 301  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Shigella Flexneri  
US-10-043-487-301

Query Match	100.0%;	Score 582;	DB 14;	Length 158;
Best Local Similarity	100.0%;	Pred. No. 1.8e-58;		
Matches 111;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AKHPSQSDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML	60	
Db	48	AKHPSQSDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML	107	
QY	61	ATWRRTPTREATLELLGVLGRVMDLLGCLDIEEALCGPAALPPAPSLLR	111	
Db	108	ATWRRTPTREATLELLGVLGRVMDLLGCLDIEEALCGPAALPPAPSLLR	158	
RESULT 2				
US-10-349-977-37				
; Sequence 37, Application US/10349977				

Publication No. US20040013646A1  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
BOLDIN, Mark  
METT, Igor  
VARFOLOMEYEV, Eugene  
TITLE OF INVENTION: MODULATOR OF TNF/NGF SUPERFAMILY RECEPTORS  
AND SOLUBLE OLIGOMERIC TNF/NGF SUPERFAMILY RECEPTORS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/349,977  
FILING DATE: 24-Jan-2003  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,562  
FILING DATE: 11-MAY-1995  
APPLICATION NUMBER: PCT/US95/05854  
FILING DATE: 11-MAY-1994  
APPLICATION NUMBER: IL 109,632  
FILING DATE: 02-OCT-1994  
APPLICATION NUMBER: IL 111,125  
FILING DATE: 02-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=15A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 426 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-10-349-977-37  
Query Match 100.0%; Score 582; DB 15; Length 426;  
Best Local Similarity 100.0%; Pred. No. 5.8e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQLONGRCLEAQYSML 60  
316 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQLONGRCLEAQYSML 375  
Db  
QY 61 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111  
376 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 426  
Db  
RESULT 3  
US-10-280-047-5  
Sequence 5, Application US/10280047  
Publication No. US20030180883A1  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Rosen, Craig A  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor 10  
FILE REFERENCE: PF379P1D1  
CURRENT APPLICATION NUMBER: US/10/280,047

CURRENT FILING DATE: 2002-10-25  
PRIOR APPLICATION NUMBER: 09/580,212  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 09/086,483  
PRIOR FILING DATE: 1998-05-29  
PRIOR APPLICATION NUMBER: 60/069,112  
PRIOR FILING DATE: 1997-12-09  
PRIOR APPLICATION NUMBER: 60/050,936  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: 60/144,023  
PRIOR FILING DATE: 1999-07-15  
PRIOR APPLICATION NUMBER: 60/142,563  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: 60/136,786  
PRIOR FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 453  
TYPE: PRT  
ORGANISM: human  
US-10-280-047-5  
Query Match 100.0%; Score 582; DB 14; Length 453;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQLONGRCLEAQYSML 60  
343 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQLONGRCLEAQYSML 402  
Db  
QY 61 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111  
403 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 453  
Db  
RESULT 4  
US-09-826-212-3  
Sequence 3, Application US/09826212  
Patent No. US20010021516A1  
GENERAL INFORMATION:  
APPLICANT: Wei, Ying-Fei  
APPLICANT: Gentz, Reiner  
APPLICANT: Ruben, Steven  
APPLICANT: Ni, Jian  
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
FILE REFERENCE: 1488.1280006  
CURRENT APPLICATION NUMBER: US/09/826,212  
CURRENT FILING DATE: 2001-04-05  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-826-212-3  
Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQLONGRCLEAQYSML 60  
345 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQLONGRCLEAQYSML 404  
Db  
QY 61 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111  
405 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455  
Db  
RESULT 5  
US-09-333-966-5  
Sequence 5, Application US/09333966

Patent No. US20020009773A1  
GENERAL INFORMATION:  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ni, Jian  
APPLICANT: Dixit, Vishva  
APPLICANT: Gentz, Reiner L.  
APPLICANT: Dillon, Patrick J.  
TITLE OF INVENTION: Death Domain Containing Receptors  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., NW, Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/333,966  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/815,469  
FILING DATE:  
FILING DATE: 06-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/028,711  
FILING DATE: 17-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/013,285  
FILING DATE: 12-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
STRANDEDNESS: No. US20020009773A1 Relevant  
TOPOLOGY: No. US20020009773A1 Relevant  
MOLECULE TYPE: protein  
US-09-333-966-5

Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSQSLDTPATLYAVVNPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQAQY SML 60  
DB 345 AHKPSQSLDTPATLYAVVNPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQAQY SML 404  
QY 61 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111  
DB 405 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 6  
US-09-027-287-3  
Sequence 3, Application US/09027287A  
Patent No. US20020064869A1  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ruben, Steven M.

APPLICANT: Ullrich, Stephen  
TITLE OF INVENTION: Apoptosis Inducing Molecule II  
FILE REFERENCE: 1488.0650004  
CURRENT APPLICATION NUMBER: US/09/027,287A  
CURRENT FILING DATE: 1998-02-20  
EARLIER APPLICATION NUMBER: US 09/003,886  
EARLIER FILING DATE: 1998-01-07  
EARLIER APPLICATION NUMBER: US 08/822,953  
EARLIER FILING DATE: 1997-03-21  
EARLIER APPLICATION NUMBER: US 60/030,157  
EARLIER FILING DATE: 1996-10-31  
EARLIER APPLICATION NUMBER: US 60/013,923  
EARLIER FILING DATE: 1996-03-22  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-027-287-3

Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSQSLDTPATLYAVVNPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQAQY SML 60  
DB 345 AHKPSQSLDTPATLYAVVNPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQAQY SML 404  
QY 61 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111  
DB 405 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 7  
US-09-874-138-3  
Sequence 3, Application US/09874138  
Patent No. US20020072091A1  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Gentz, Reiner L.  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: Death Domain Containing Receptor 5  
FILE REFERENCE: 1488.1310006  
CURRENT APPLICATION NUMBER: US/09/874,138  
CURRENT FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 09/565,009  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: 60/148,939  
PRIOR FILING DATE: 1999-08-13  
PRIOR APPLICATION NUMBER: 60/133,238  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: 60/132,498  
PRIOR FILING DATE: 1999-05-04  
PRIOR APPLICATION NUMBER: 09/042,583  
PRIOR FILING DATE: 1998-03-17  
PRIOR APPLICATION NUMBER: 60/054,021  
PRIOR FILING DATE: 1997-07-29  
PRIOR APPLICATION NUMBER: 60/040,846  
PRIOR FILING DATE: 1997-03-17  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-874-138-3

Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLTDTPATLYAVVENPPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML 60  
DB 345 AHKPSLTDTPATLYAVVENPPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML 404  
QY 61 ATWRRTPREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPAPSLR 111  
DB 405 ATWRRTPREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPAPSLR 455

RESULT 8  
US-09-840-707A-16  
; Sequence 16, Application US/09840707A  
; Patent No. US20020077276A1  
; GENERAL INFORMATION:  
; APPLICANT: Fredeking, Terry M.  
; APPLICANT: Ignatyev, George M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS  
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS  
; FILE REFERENCE: 24881-301C  
; CURRENT APPLICATION NUMBER: US/09/840,707A  
; CURRENT FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: 09/562,979  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/198,210  
; PRIOR FILING DATE: 1999-04-27  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Tumor Necrosis Factor p55 Receptor  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AAA36753/GenBank  
; DATABASE ENTRY DATE: 1995-08-03  
US-09-840-707A-16

Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLTDTPATLYAVVENPPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML 60  
DB 345 AHKPSLTDTPATLYAVVENPPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML 404  
QY 61 ATWRRTPREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPAPSLR 111  
DB 405 ATWRRTPREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPAPSLR 455

RESULT 9  
US-09-252-656B-3  
; Sequence 3, Application US/09252656B  
; Patent No. US20020081647A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ruben, Steven M.  
; APPLICANT: Zhang, Jun  
; APPLICANT: Ullrich, Stephen  
; APPLICANT: Zhai, Yifan  
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
; FILE REFERENCE: 1488.065006  
; CURRENT APPLICATION NUMBER: US/09/252,656B  
; CURRENT FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: US 60/075,409  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: US 09/027,287  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: US 09/003,886  
; PRIOR FILING DATE: 1998-01-07  
; PRIOR APPLICATION NUMBER: US 08/822,953

QY 1 AHKPSLTDTPATLYAVVENPPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML 60  
DB 345 AHKPSLTDTPATLYAVVENPPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML 404  
QY 61 ATWRRTPREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPAPSLR 111  
DB 405 ATWRRTPREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPAPSLR 455

RESULT 10  
US-09-899-422-2  
; Sequence 2, Application US/09899422  
; Patent No. US20020090676A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmler, Adolph  
; APPLICANT: Maurer-Fogy, Ingrid  
; APPLICANT: Stratzowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; FILE REFERENCE: 98,385-H  
; CURRENT APPLICATION NUMBER: US/09/899,422  
; CURRENT FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: 09/525,998  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-899-422-2

Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLTDTPATLYAVVENPPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML 60  
DB 345 AHKPSLTDTPATLYAVVENPPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML 404  
QY 61 ATWRRTPREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPAPSLR 111  
DB 405 ATWRRTPREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPAPSLR 455

RESULT 11  
US-09-899-422-17

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; Sequence 17, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
; OTHER INFORMATION: 1TNF-R2
; US-09-899-422-17

Query Match 100.0%; Score 582; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 6.3e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQNGRCLREAQYSML 60
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQNGRCLREAQYSML 404

QY 61 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 111
Db 405 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 12
US-09-935-727-5
; Sequence 5, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-727-5

Query Match 100.0%; Score 582; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 6.3e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQNGRCLREAQYSML 60
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQNGRCLREAQYSML 404

QY 61 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 111
Db 405 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 13
US-09-898-234-2
; Sequence 2, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-898-234-2

Query Match 100.0%; Score 582; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 6.3e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQNGRCLREAQYSML 60
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQNGRCLREAQYSML 404

QY 61 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 111
Db 405 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 455
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RESULT 14  
US-09-898-234-17  
; Sequence 17, Application US/09898234  
; Patent No. US2002015112A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmler, Adolph  
; APPLICANT: Maurer-Poggy, Ingrid  
; APPLICANT: Stratos, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; FILE OF INVENTION: Them  
; FILE REFERENCE: 98,385-I  
; CURRENT APPLICATION NUMBER: US/09/898,234  
; CURRENT FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 09/525,998  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in  
; OTHER INFORMATION: LTNF-R2  
US-09-898-234-17

Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML 60  
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML 404  
QY 61 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPALPPAPSLLR 111  
Db 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPALPPAPSLLR 455

RESULT 15  
US-09-756-854-5  
; Sequence 5, Application US/09756854  
; Patent No. US20020164684A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; Yu, Guo-Liang  
; Fan, Ping  
; Gentz, Reiner  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/756,854

FILING DATE: 10-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/095,094  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoover, Kenley K.  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PF375  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-756-854-5  
Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML 60  
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLQNGRCLEAQSML 404  
QY 61 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPALPPAPSLLR 111  
Db 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPALPPAPSLLR 455

Search completed: June 1, 2004, 14:50:04  
Job time : 36.8922 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:37:07 ; Search time 11.6317 Seconds  
(without alignments)  
917.942 Million cell updates/sec

Title: US-09-854-906-8

Perfect score: 582

Sequence: 1 AHKPSQLDTPATLYAVVE.....DIEALCGPALPPAPSLLR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	582	100.0	455	1	GQHTU1
2	462.5	79.5	461	2	tumor necrosis fac
3	386	66.3	461	1	GQRT11
4	350.5	60.2	454	1	GQMS11
5	91.5	15.7	671	2	serine/threonine p
6	90	15.5	656	2	receptor interacti
7	86	14.8	1848	2	ankyrin, erythrocy
8	86	14.8	1862	2	ankyrin - mouse
9	82	14.1	163	2	probable methylmal
10	80.5	13.8	1765	2	ankyrin 3, splice
11	80.5	13.8	1940	2	ankyrin 3, splice
12	80.5	13.8	1943	2	ankyrin 3, splice
13	80.5	13.8	1961	2	ankyrin 3, splice
14	80.5	13.8	4377	2	ankyrin 3, long sp
15	80	13.7	1856	2	ankyrin 1, erythro
16	80	13.7	1880	2	ankyrin 1, erythro
17	80	13.7	1881	1	aminotransferase,
18	78.5	13.5	388	2	activator of Hsp70
19	77.5	13.3	591	2	hypothetical prote
20	77.5	13.3	591	2	acetyl-coenzyme A
21	77	13.2	316	2	ankyrin, erythrocy
22	75.5	13.0	138	2	FADD protein - hum
23	74.5	12.8	208	2	aminotransferase (
24	74.5	12.8	388	2	Gene hb protein -
25	74.5	12.8	426	2	ankyrin 2, neurona
26	74.5	12.8	3924	2	probable ATP-bindi
27	74	12.7	536	2	conserved hypothet
28	72.5	12.5	295	2	glutaminyl-tRNA sy
29	72.5	12.5	580	2	G82693

#### ALIGNMENTS

##### RESULT 1

GQHTU1

tumor necrosis factor receptor 1 precursor [validated] - human

N;Alternate names: F55 tumor necrosis factor receptor; TNF receptor type 1

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 08-Dec-2000

C;Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38

R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmeler, A.; Ambros, P.F.

Genomics 13, 219-224, 1992

A;Title: Structure of the human TNF receptor 1 (p50) gene (TNFRF1) and localization to ch

A;Reference number: A38208; MUID:92250049; PMID:1315717

A;Accession: A38208

A;Molecule type: DNA

A;Residues: 1-455 <FUC>

A;Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:G339748; PIDN:AAA61201.1; PID:9

R;Loetscher, H.; Pan, Y.C.B.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau

Cell 61, 351-359, 1990

A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep

A;Reference number: A34899; MUID:90235284; PMID:2158862

A;Accession: A34899

A;Molecule type: mRNA

A;Residues: 1-455 <LOE>

A;Cross-references: GB:M58286; GB:M33480; NID:G339753; PIDN:AAA36753.1; PID:G339754

A;Experimental source: placenta

A;Note: part of this sequence, including the amino end of the mature protein, confirmed

R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.

Cell 61, 361-370, 1990

A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.

A;Reference number: A34900; MUID:90235285; PMID:2158863

A;Accession: A34900

A;Molecule type: mRNA

A;Residues: 1-455 <SCH>

A;Cross-references: GB:M33294; NID:G339744; PIDN:AAA03210.1; PID:G339745

R;Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pflizenmaier, K.; Lantz, M.;

DNA Cell Biol. 9, 705-715, 1990

A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto

A;Reference number: A36555; MUID:91090841; PMID:1702293

A;Accession: A36555

A;Molecule type: mRNA

A;Residues: 1-455 <HIM>

A;Cross-references: GB:M63121; NID:G339755; PIDN:AAA36754.1; PID:G339756

A;Accession: C36555

A;Molecule type: protein

A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;107-128;162-167,'X',169-2

A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble

R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.

Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990

A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re

A;Reference number: A38281; MUID:91017509; PMID:2170974

A;Accession: A38281

A;Molecule type: mRNA

A;Residues: 1-455 <GRA>  
A;Cross-references: GB:M37764  
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372  
R;Nopnar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zhang, R.; Aderka, D.; Holtmann-EMBO J. 9, 3269-3278, 1990  
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I form of the receptor.  
A;Reference number: S12057; PMID:91006021; PMID:1698610  
A;Accession: S12057  
A;Molecule type: mRNA  
A;Residues: 1-455 <NOP>  
A;Cross-references: EMBL:X55113; NID:g37223; PIDN:CAA39021.1; PID:g37224  
A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, were  
R;Kemper, O.; Wallach, D.  
Gene 134, 209-216, 1993  
A;Title: Cloning and partial characterization of the promoter for the human p55 tumor necrosis factor receptor.  
A;Reference number: J70758; PMID:94085779; PMID:8262379  
A;Accession: J70758  
A;Molecule type: DNA  
A;Residues: 1-13 <KEM>  
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayar, J.M.  
Eur. J. Immunol. 20, 1167-1174, 1990  
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence and characterization of an inhibitor (soluble tumor necrosis factor receptor).  
A;Reference number: A60231; PMID:90292116; PMID:2113477  
A;Accession: A60231  
A;Molecule type: protein  
A;Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>  
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor receptor).  
A;Reference number: A38258; PMID:91062364; PMID:2174164  
A;Accession: A38258  
A;Molecule type: protein  
A;Residues: 41-60 <GAT>  
A;Experimental source: cancer patient serum  
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetere, C.; Thysell, H.; Grubb, A.; Adolf, G.  
Eur. J. Haematol. 42, 270-275, 1989  
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from human urine.  
A;Reference number: A60594; PMID:89171156; PMID:2924890  
A;Accession: A60594  
A;Molecule type: protein  
A;Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>  
A;Experimental source: renal failure patient urine  
R;Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for two distinct receptors.  
A;Reference number: A35010; PMID:90110215; PMID:2153136  
A;Accession: A35010  
A;Molecule type: protein  
A;Residues: 41-45 <ENG>  
A;Experimental source: normal urine  
R;Kajihara, J.; Asada, A.; Kirihaara, S.; Kato, K.  
Biochem. Biotechnol. 58, 2266-2268, 1994  
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.  
A;Reference number: JC2404; PMID:95128033; PMID:7765720  
A;Accession: JC2404  
A;Molecule type: protein  
A;Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>  
A;Experimental source: urine  
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).  
A;Gene: GDB:TNFR1  
A;Cross-references: GDB:125913; OMIM:191190  
A;Map position: 12p13.2-12p13.2  
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-45/Domain: signal sequence #status predicted <MAT>  
F;30-211/Domain: extracellular #status predicted <EXT>  
F;41-201/Domain: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status predicted <EXT>  
F;44-82/Domain: NGF receptor repeat homology <NG1>

F;84-126/Domain: NGF receptor repeat homology <NG2>  
F;127-167/Domain: NGF receptor repeat homology <NG3>  
F;168-196/Domain: NGF receptor repeat homology <NG4>  
F;212-234/Domain: transmembrane #status predicted <INT>  
F;235-455/Domain: intracellular #status predicted <EXT>  
F;54,145,151/Binding site: carboxylate (Asn) (covalent) #status predicted  
Query Match 100.0%; Score 582; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.3e-52;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKQSLDTPATLYAVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQAQSM 60  
DB 345 AHKQSLDTPATLYAVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQAQSM 404  
QY 61 ATWRRTPRREATLELLGRVLRDMDLGLCLEDIEALCGPAALPPAPSLLR 111  
DB 405 ATWRRTPRREATLELLGRVLRDMDLGLCLEDIEALCGPAALPPAPSLLR 455  
RESULT 2  
JC4302  
tumor necrosis factor receptor p55 precursor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Jul-1999  
C;Accession: JC4302; PC4093  
R;Suter, B.; Pauli, U.  
Gene 163, 263-266, 1995  
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.  
A;Reference number: JC4302; MUID:96011645; PMID:7590278  
A;Accession: JC4302  
A;Molecule type: mRNA  
A;Residues: 1-461 <SUT>  
A;Cross-references: GB:U19994; NID:gl141752; PIDN:AA48499.1; PID:gl141753  
A;Accession: PC4093  
A;Molecule type: protein  
A;Residues: 1-7 <SU2>  
A;Experimental source: kidney cell line 15  
C;Genetics:  
A;Gene: tnfr  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>  
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>  
F;44-82/Domain: NGF receptor repeat homology <NG1>  
F;84-126/Domain: NGF receptor repeat homology <NGF>  
F;211-231/Domain: transmembrane #status predicted <TMM>  
F;235-455/Domain: signal transduction #status predicted <SIT>  
F;54,145,151/Binding site: carboxylate (Asn) (covalent) #status predicted  
Query Match 79.5%; Score 462.5; DB 2; Length 461;  
Best Local Similarity 83.0%; Pred. No. 3.4e-40;  
Matches 93; Conservative 3; Mismatches 15; Indels 1; Gaps 1;  
QY 1 AHK-QSLDTPATLYAVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQAQSM 59  
DB 350 AHSAPQAQLADADPATLYAVDVGVPPTRWKEFVRRGLSEHEIERLEQLQNGRCLEAQAQSM 409  
QY 60 LATWRRTPRREATLELLGRVLRDMDLGLCLEDIEALCGPAALPPAPSLLR 111  
DB 410 LAEWRRTPRREATLELLGRVLRDMDLGLCLEDIEALCGPAALPPAPSLLR 461  
RESULT 3  
GQRT1  
tumor necrosis factor receptor 1 precursor - rat  
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1992 #sequence\_revision 07-Oct-1994 #text\_change 22-Jun-1999  
C;Accession: B36555  
R;Himmeler, A.; Maurer-Poggy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; DNA Cell Biol. 9, 705-715, 1990

A;Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor  
 A;Reference number: A36555; MUID:91090841; PMID:1702293  
 A;Accession: B36555  
 A;Molecule type: mRNA  
 A;Residues: 1-461 <HM>  
 A;Cross-references: GB:M63122; NID:G207361; PIDN:AAA42256.1; PID:G207362  
 C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).  
 C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C;Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F;1-29/Domain: signal sequence #status predicted <SIG>  
 F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
 F;30-211/Domain: extracellular #status predicted <EXT>  
 F;30-201/Product: tumor necrosis factor binding protein #status predicted <TPP>  
 F;44-82/Domain: NGF receptor repeat homology <NG1>  
 F;84-126/Domain: NGF receptor repeat homology <NG2>  
 F;127-167/Domain: NGF receptor repeat homology <NG3>  
 F;168-204/Domain: NGF receptor repeat homology <NG4>  
 F;212-234/Domain: transmembrane #status predicted <MEM>  
 F;235-461/Domain: intracellular #status predicted <INT>  
 F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.3%; Score 386; DB 1; Length 461;  
 Best Local Similarity 73.3%; Pred. No. 2.9e-32;  
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QY 1 AHKPSQLDTPATLVAVVENVPLRWKVFRLGLSDHEIDRLQNGRCLEAAYSM 60  
 Db 352 AAQPSQLDTPATLVAVVENVPLRWKVFRLGLSDHEIDRLQNGRCLEAAYSM 411

QY 61 ATWRRTPREATLELLGRVLRMDLLGLCLEDIEEALCGPA 101  
 Db 412 EAWRRTPREATLELLGRVLRMDLLGLCLEDIEEALCGPA 452

RESULT 4  
 GQWST1  
 tumor necrosis factor receptor 1 precursor - mouse  
 N;Alternate names: tumor necrosis factor receptor, 55K  
 C;Species: Mus musculus (house mouse)  
 C;Date: 30-Jun-1992 #sequence revision 10-Jun-1992 #text change 01-Dec-2000  
 C;Accession: A38634; B40254; S16677; S19021; I54532; I57826  
 R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E. Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
 A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors  
 A;Reference number: A38634; MUID:91187885; PMID:1849278  
 A;Accession: A38634  
 A;Molecule type: mRNA  
 A;Residues: 1-454 <LEW>  
 A;Cross-references: GB:M60468; NID:G199825; PIDN:AAA39751.1; PID:G199826  
 R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk Mol. Cell. Biol. 11, 3020-3026, 1991  
 A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for TNF  
 A;Reference number: A40254; MUID:91246168; PMID:1645445  
 A;Accession: B40254  
 A;Molecule type: mRNA  
 A;Residues: 1-454 <GO2>  
 A;Cross-references: GB:M60468; NID:G199825; PIDN:AAA39751.1; PID:G199826  
 R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissenerghis, A.M.; Gray, P.W.; Feldman Eur. J. Immunol. 21, 1649-1656, 1991  
 A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor  
 A;Reference number: S16677; MUID:91285014; PMID:1647956  
 A;Accession: S16677  
 A;Molecule type: mRNA  
 A;Residues: 1-454 <BAR>  
 A;Cross-references: EMBL:X59238; NID:G53578; PIDN:CAA41922.1; PID:G53579  
 R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W. Immunogenetics 34, 338-340, 1991  
 A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.  
 A;Reference number: S19021; MUID:92039815; PMID:1657766  
 A;Accession: S19021  
 A;Molecule type: mRNA  
 A;Residues: 1-454 <ROT>  
 A;Cross-references: EMBL:X57796; NID:G54848; PIDN:CAA40936.1; PID:G54849

R;Bebo, B.F. Immunogenetics 39, 450-451, 1994  
 A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1  
 A;Reference number: I54532; MUID:94245292; PMID:8188324  
 A;Accession: I54532  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-454 <RES>  
 A;Cross-references: GB:I26349; NID:G430732; PIDN:AAA59361.1; PID:G430733  
 R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M. Mol. Immunol. 30, 165-176, 1993  
 A;Title: Genomic organization and promoter function of the murine tumor necrosis factor gene  
 A;Reference number: I57826; MUID:93156721; PMID:8381516  
 A;Accession: I57826  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-393, G', 395-454 <RE2>  
 A;Cross-references: GB:M76656; NID:G202100; PIDN:AAA40465.1; PID:G202102  
 C;Comment: This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).  
 C;Gene: TNFR-2  
 A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1  
 C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protein  
 F;1-29/Domain: signal sequence #status predicted <SIG>  
 F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
 F;30-212/Domain: extracellular #status predicted <EXT>  
 F;44-82/Domain: NGF receptor repeat homology <NG1>  
 F;84-126/Domain: NGF receptor repeat homology <NG2>  
 F;127-167/Domain: NGF receptor repeat homology <NG3>  
 F;168-204/Domain: NGF receptor repeat homology <NG4>  
 F;213-235/Domain: transmembrane #status predicted <MEM>  
 F;236-454/Domain: intracellular #status predicted <INT>  
 F;54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 60.2%; Score 350.5; DB 1; Length 454;  
 Best Local Similarity 69.3%; Pred. No. 1.4e-28;  
 Matches 70; Conservative 10; Mismatches 20; Indels 1; Gaps 1;

QY 1 AHKPSQLDTPATLVAVVENVPLRWKVFRLGLSDHEIDRLQNGRCLEAAYSM 60  
 Db 346 AH-PQSPDNADIALLVAVVGVPPAPKRFMPGUSEHEIERLEWNGRCLEAAYSM 404

QY 61 ATWRRTPREATLELLGRVLRMDLLGLCLEDIEEALCGPA 101  
 Db 405 EAWRRTPREATLELLGRVLRMDLLGLCLEDIEEALCGPA 445

RESULT 5  
 T09479  
 serine/threonine protein kinase (EC 2.7.1.1-) RIP - human  
 C;Species: Homo sapiens (man)  
 C;Date: 16-Jul-1999 #sequence revision 16-Jul-1999 #text change 17-Nov-2000  
 C;Accession: T09479; I38992  
 R;Huang, J.; Hau, H.; Baichwal, V.R.; Goeddel, D.V. submitted to the EMBL Data Library, August 1998  
 A;Reference number: Z15685  
 A;Accession: T09479  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-671 <HUA>  
 A;Cross-references: EMBL:U50062; NID:G3426026; PID:G3426027  
 R;Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B. Cell 81, 513-523, 1995  
 A;Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1 (CD95)  
 A;Reference number: A56913; MUID:95277838; PMID:7538908  
 A;Accession: I38992  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 300-513, 'S', 515-671 <RES>  
 A;Cross-references: EMBL:U25994; NID:G829616; PIDN:AAAC50137.1; PID:G829617  
 C;Gene: RIP

RESULT 7  
S37771  
ankyrin, erythrocyte - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 27-May-1994 #sequence\_revision 03-Aug-1995 #text\_change 13-Aug-1999  
C:Accession: S37771  
R:J.Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.  
J. Biol. Chem. 268, 9533-9540, 1993  
A:Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found am  
A:Reference number: S37771; MUID:93252825; PMID:8486643  
A:Accession: S37771  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1848 <BR>  
A:Cross-references: EMBL:X69063; NID:g311816; PIDN:CAA48801.1; PID:g311817  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing  
F:48-80/Domain: ankyrin repeat homology <AN01>  
F:81-113/Domain: ankyrin repeat homology <AN02>  
F:114-146/Domain: ankyrin repeat homology <AN03>  
F:147-175/Domain: ankyrin repeat homology <AN04>  
F:176-208/Domain: ankyrin repeat homology <AN05>  
F:209-241/Domain: ankyrin repeat homology <AN06>  
F:242-274/Domain: ankyrin repeat homology <AN07>  
F:275-307/Domain: ankyrin repeat homology <AN08>

```

F;308-340/Domain: ankysin repeat homology <AN09>  

F;341-373/Domain: ankysin repeat homology <AN10>  

F;374-406/Domain: ankysin repeat homology <AN11>  

F;407-439/Domain: ankysin repeat homology <AN12>  

F;440-472/Domain: ankysin repeat homology <AN13>  

F;473-505/Domain: ankysin repeat homology <AN14>  

F;506-538/Domain: ankysin repeat homology <AN15>  

F;539-571/Domain: ankysin repeat homology <AN16>  

F;572-604/Domain: ankysin repeat homology <AN17>  

F;605-637/Domain: ankysin repeat homology <AN18>  

F;638-670/Domain: ankysin repeat homology <AN19>  

F;671-703/Domain: ankysin repeat homology <AN20>  

F;704-736/Domain: ankysin repeat homology <AN21>  

F;737-769/Domain: ankysin repeat homology <AN22>  

F;770-802/Domain: ankysin repeat homology <AN23>  
  

Query Match      14.8%; Score 86; DB 2; Length 1848;  

Best Local Similarity 23.4%; Pred.No. 2;  

Matches 32; Conservative 19; Mismatches 48; Indels 38; Gaps 4;  
  

QY    8   DTDPPATLYAVVENVPFLKWKPFVRLGLGSDHIDLELQNGRCLREAQYSMLATWRRRT 67  

       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :  

Db     1411 DTDIVEMRVAVTREHLGLSWAEIARELOFSVEDINRKIRVENPNSLLDQSALLTLKWDR - 1469  

               ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :  

QY    68 PRREATLELGRVRDMD---LIGCLE-----DI 93  

       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :  

Db     1470 EGENAKMENLTALRIDNRSEINVMLEVSGRGQRNLKPERRHGHDREYSLSPSQVNGYSSL 1529  

               ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :  

QY    94 EEALCGPALP---RAP 107  

       ::| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :  

Db     1530 QDELLPASLOYALPSP 1546  

               ::| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :  
  

RESULT 8  

I49502  

ankyrin - mouse  

C;Species: Mus musculus (house mouse)  

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999  

C;Accession: I49502  

R;White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.  

Mamm. Genome 3, 281-285, 1992  

A;Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory do  

A;Reference number: I49502; UID:I49502; PMID:1386265  

A;Status: preliminary; translated from GB/EMBL/DDBB  

A;Molecule type: mRNA  

A;Residues: 1-1862 <RES>  

A;Cross-references: GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:g191940  

C;Genetics:  

A;Gene: Ank-1  

C;Superfamily: ankysin; ankysin repeat homology  

C;Keywords: alternative splicing  

F;40-72/Domain: ankysin repeat homology <AN01>  

F;73-105/Domain: ankysin repeat homology <AN02>  

F;106-138/Domain: ankysin repeat homology <AN03>  

F;139-167/Domain: ankysin repeat homology <AN04>  

F;168-200/Domain: ankysin repeat homology <AN05>  

F;201-233/Domain: ankysin repeat homology <AN06>  

F;234-266/Domain: ankysin repeat homology <AN07>  

F;267-299/Domain: ankysin repeat homology <AN08>  

F;300-332/Domain: ankysin repeat homology <AN09>  

F;333-365/Domain: ankysin repeat homology <AN10>  

F;366-398/Domain: ankysin repeat homology <AN11>  

F;399-431/Domain: ankysin repeat homology <AN12>  

F;432-464/Domain: ankysin repeat homology <AN13>  

F;465-497/Domain: ankysin repeat homology <AN14>  

F;498-530/Domain: ankysin repeat homology <AN15>  

F;531-563/Domain: ankysin repeat homology <AN16>  

F;564-596/Domain: ankysin repeat homology <AN17>  

F;597-629/Domain: ankysin repeat homology <AN18>  

F;630-662/Domain: ankysin repeat homology <AN19>  

F;663-695/Domain: ankysin repeat homology <AN20>  

F;696-728/Domain: ankysin repeat homology <AN21>  


```



## C:Genetics:

A:Gene: Ank3  
A:Map position: 10  
A:Introns: 855/1  
A:Function:

## C:Description:

A:Description: supposed to play an important role in the polarized distribution of many  
A:Note: major kidney ankyrin  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing

Query Match 13.8%; Score 80.5; DB 2; Length 1943;

Best Local Similarity 29.8%; Pred. No. 7.8;

Matches 25; Conservative 14; Mismatches 40; Indels 5; Gaps 2;

QY 17 AVVENPPLRWKEFVRRLGSLDHEIDRLQNGRCLEAQYSMLATWRRTPRRATLEL 76

DB 1465 AIVADHLGLSWTELARELNFVSDEINQIRVENPNSLSQSFMLKKWVTR-DGKNATTDA 1523

QY 77 LGRVLRMDLLGCLDIEALCGP 100

DB 1524 LTVSLTKINRI-----DIVTLLEGP 1543

## RESULT 13

T42716

C:Species: Mus musculus (house mouse)

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 04-Mar-2000

C:Accession: T42716

R:Pieters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.

J. Cell Biol. 130, 313-330, 1995

A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene  
the repeat domain.  
A:Reference number: Z22237; MUID:95340633; PMID:7615634

A:Accession: T42716

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1961 <PEP>

A:Cross-references: EMBL:L40632; NID:g710548; PID:g710552; PIDN:AA01607.1

A:Experimental source: strain C57BL/6J; kidney

## C:Genetics:

A:Gene: Ank3

A:Map position: 10

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

Query Match 13.8%; Score 80.5; DB 2; Length 1961;

Best Local Similarity 29.8%; Pred. No. 7.9;

Matches 25; Conservative 14; Mismatches 40; Indels 5; Gaps 2;

QY 17 AVVENPPLRWKEFVRRLGSLDHEIDRLQNGRCLEAQYSMLATWRRTPRRATLEL 76

DB 1483 AIVADHLGLSWTELARELNFVSDEINQIRVENPNSLSQSFMLKKWVTR-DGKNATTDA 1541

QY 77 LGRVLRMDLLGCLDIEALCGP 100

DB 1542 LTVSLTKINRI-----DIVTLLEGP 1561

## RESULT 14

A55575

ankyrin 3, long splice form - human

N:Alternate names: ankyrin G

C:Species: Homo sapiens (man)

C:Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 20-Sep-1999

C:Accession: A55575

R:Kordali, E.; Lambert, S.; Bennett, V.

J. Biol. Chem. 270, 2352-2359, 1995

A:Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the ax

A:Reference number: A55575; MUID:95138209; PMID:7836469

A:Accession: A55575

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-4377 <KOR>

A:Cross-references: GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025

## C:Genetics:

A:Gene: GDB:ANK3

A:Cross-references: GDB:424503; OMIM:600465

A:Map position: 10q21-10q21

C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

C:Keywords: alternative splicing; peripheral membrane protein

F:73-105/Domain: ankyrin repeat homology <AN01>

F:106-138/Domain: ankyrin repeat homology <AN02>

F:139-171/Domain: ankyrin repeat homology <AN03>

F:172-200/Domain: ankyrin repeat homology <AN04>

F:201-233/Domain: ankyrin repeat homology <AN05>

F:234-266/Domain: ankyrin repeat homology <AN06>

F:267-299/Domain: ankyrin repeat homology <AN07>

F:300-332/Domain: ankyrin repeat homology <AN08>

F:333-365/Domain: ankyrin repeat homology <AN09>

F:366-398/Domain: ankyrin repeat homology <AN10>

F:399-431/Domain: ankyrin repeat homology <AN11>

F:432-464/Domain: ankyrin repeat homology <AN12>

F:465-497/Domain: ankyrin repeat homology <AN13>

F:498-530/Domain: ankyrin repeat homology <AN14>

F:531-563/Domain: ankyrin repeat homology <AN15>

F:564-596/Domain: ankyrin repeat homology <AN16>

F:597-629/Domain: ankyrin repeat homology <AN17>

F:630-662/Domain: ankyrin repeat homology <AN18>

F:663-695/Domain: ankyrin repeat homology <AN19>

F:696-728/Domain: ankyrin repeat homology <AN20>

F:729-761/Domain: ankyrin repeat homology <AN21>

F:762-794/Domain: ankyrin repeat homology <AN22>

F:795-827/Domain: ankyrin repeat homology <AN23>

Query Match 13.8%; Score 80.5; DB 2; Length 4377;

Best Local Similarity 29.8%; Pred. No. 20;

Matches 25; Conservative 14; Mismatches 40; Indels 5; Gaps 2;

QY 17 AVVENPPLRWKEFVRRLGSLDHEIDRLQNGRCLEAQYSMLATWRRTPRRATLEL 76

DB 4095 AIVADHLGLSWTELARELNFVSDEINQIRVENPNSLSQSFMLKKWVTR-DGKNATTDA 4153

QY 77 LGRVLRMDLLGCLDIEALCGP 100

DB 4154 LTVSLTKINRI-----DIVTLLEGP 4173

## RESULT 15

B35049

ankyrin 1, erythrocyte splice form 3 - human

N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

C:Contains: ankyrin 2.2, erythrocyte

C:Species: Homo sapiens (man)

C:Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 10-Jul-1998

R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.;

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A:Title: cDNA sequence for human erythrocyte ankyrin.

A:Reference number: A35049; MUID:90175370; PMID:1689849

A:Accession: B35049

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1856 <LAM>

## C:Genetics:

A:Gene: GDB:ANK1; ANK

A:Cross-references: GDB:118737; OMIM:182900

A:Map position: 8p11.2-8p11.2

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

F:2-1513/Domain: ankyrin 1, erythrocyte form 3 #status predicted <MAT>

F:2-1513/Domain: ankyrin 1, erythrocyte form 3 #status predicted <MAT>

F:44-76/Domain: ankyrin repeat homology <AN01>

F:77-109/Domain: ankyrin repeat homology <AN02>

F:110-142/Domain: ankyrin repeat homology <AN03>

F:143-171/Domain: ankyrin repeat homology <AN04>

F;172-204/Domain: ankyrin repeat homology <AN05>  
F;205-237/Domain: ankyrin repeat homology <AN06>  
F;238-270/Domain: ankyrin repeat homology <AN07>  
F;271-303/Domain: ankyrin repeat homology <AN08>  
F;304-336/Domain: ankyrin repeat homology <AN09>  
F;337-369/Domain: ankyrin repeat homology <AN10>  
F;370-402/Domain: ankyrin repeat homology <AN11>  
F;403-435/Domain: ankyrin repeat homology <AN12>  
F;436-468/Domain: ankyrin repeat homology <AN13>  
F;469-501/Domain: ankyrin repeat homology <AN14>  
F;502-534/Domain: ankyrin repeat homology <AN15>  
F;535-567/Domain: ankyrin repeat homology <AN16>  
F;568-600/Domain: ankyrin repeat homology <AN17>  
F;601-633/Domain: ankyrin repeat homology <AN18>  
F;634-666/Domain: ankyrin repeat homology <AN19>  
F;667-699/Domain: ankyrin repeat homology <AN20>  
F;700-732/Domain: ankyrin repeat homology <AN21>  
F;733-765/Domain: ankyrin repeat homology <AN22>  
F;766-798/Domain: ankyrin repeat homology <AN23>

Query Match 13.7%; Score 80; DB 2; Length 1856;  
Best Local Similarity 30.1%; Pred. No. 8.4;  
Matches 25; Conservative 14; Mismatches 42; Indels 2; Gaps 2;  
  
Qy 4 PQSLDTPDPAFL-YAVVENVPLRWKFEVRLGLSDHEIDRLQLNGRCLEAQQYSLAT 62  
Db 1394 PGSLSGTEQAEMKXAVISEHGLSWAELARELQFVEDINEIRVENPNSLLEQSVALLNL 1453  
  
Qy 63 WRRTPPREATLELLGRVLRMD 85  
Db 1454 WVIR-EGONANNNLYTALQSID 1475

Search completed: June 1, 2004, 14:47:08  
Job time : 11.6317 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 .Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 14:33:56 ; Search time 7.97605 Seconds  
(without alignments)  
724.643 Million cell updates/sec

Title: US-09-854-906-8

Perfect score: 582

Sequence: 1 AHKPSLDTDDPATLYAVVE.....DIEALCGPAALPPAPSLLR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582	100.0	455	1	TR1A_HUMAN
2	462.5	79.5	461	1	TR1A_PIG
3	424	72.9	471	1	TR1A_BOVIN
4	386	66.3	461	1	TR1A_RAT
5	350.5	60.2	454	1	TR21A_MOUSE
6	167.5	28.8	417	1	TR25_HUMAN
7	100	17.2	381	1	TI0B_MOUSE
8	91.5	15.7	671	1	RIK1_HUMAN
9	90	15.5	656	1	RIK1_MOUSE
10	86	14.8	1862	1	ANK1_MOUSE
11	80.5	13.8	4377	1	ANK1_HUMAN
12	80	13.7	1880	1	ANK1_HUMAN
13	77.5	13.3	591	1	ST1L_SCHPO
14	76.5	13.1	440	1	TI0B_HUMAN
15	74.5	12.8	208	1	FADD_HUMAN
16	74.5	12.8	3924	1	ANK2_HUMAN
17	73	12.5	1199	1	Y173_HUMAN
18	72.5	12.5	295	1	XJ1F_LACLA
19	72.5	12.5	580	1	SYQ_XYLFA
20	70.5	12.1	580	1	SYQ_XYLFT
21	69.5	11.9	429	1	MURA_BRUME
22	69.5	11.9	1805	1	NEST_RAT
23	69.5	11.9	2390	1	SPCP_HUMAN
24	69	11.9	481	1	TPH_XENLA
25	69	11.9	1882	1	POL2_TRSVR
26	68.5	11.8	205	1	FADD_MOUSE
27	68.5	11.8	354	1	HOM1_HUMAN
28	68.5	11.8	1092	1	RMG1_MOUSE
29	68	11.7	445	1	TPH1_CHICK
30	68	11.7	521	1	ICEA_HUMAN
31	68	11.7	554	1	PYRG_CORGL
32	67.5	11.6	371	1	HEMZ_RALSO
33	67.5	11.6	468	1	TI0A_HUMAN

#### RESULT 1

ID	TR1A_HUMAN	STANDARD;	PRT;	455 AA.
AC	P19438;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)			
DE	(TNF-R1) (TNF-R1) (p55) (CD120a) [Contains: Tumor necrosis factor			
DE	binding protein 1 (TBPI)]			
GN	TNFRSF1A OR TNFR1 OR TNFRAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RA	Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,			
RA	Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;			
RA	"Molecular cloning and expression of a receptor for human tumor			
RT	necrosis factor.";			
RL	Cell 61:361-370(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=90235284; PubMed=2158862;			
RA	Leetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,			
RA	Tabuchi H., Lesslauer W.;			
RA	"Molecular cloning and expression of the human 55 kd tumor necrosis			
RT	factor receptor.";			
RL	Cell 61:351-359(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.			
RC	MEDLINE=910906021; PubMed=1698610;			
RA	Nopnar Y., Kemper O., Brakebusch C., Engelmann H., Zwarg R.,			
RA	Aderka D., Holtmann H., Wallach D.;			
RT	"Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA			
RT	for the type I TNF-R, cloned using amino acid sequence data of its			
RT	soluble form, encodes both the cell surface and a soluble form of the			
RT	receptor.";			
RL	EMBO J. 9:3269-3278(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=91090841; PubMed=1702293;			
RA	Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,			
RA	Lantz M., Olsoson I., Hauptmann R., Stratowa C., Adolf G.R.;			
RT	"Molecular cloning and expression of human and rat tumor necrosis			
RT	factor receptor chain (p60) and its soluble derivative, tumor			
RT	necrosis factor-binding protein.";			
RL	DNA Cell Biol. 9:705-715(1990).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RA	MEDLINE=91017509; PubMed=2170974;			
RA	Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;			

34	67.5	11.6	1091	1	RHG7 RAT
35	66.5	11.4	189	1	YI35 PASMU
36	66.5	11.4	323	1	LIPA AGRT5
37	66.5	11.4	332	1	TNR6 PIG
38	66.5	11.4	781	1	NANH VIBCH
39	66.5	11.4	1091	1	RHG7 HUMAN
40	66.5	11.4	2388	1	SPCP RAT
41	66	11.3	887	1	PMC2 MOUSE
42	66	11.3	1618	1	NEST_HUMAN
43	65.5	11.3	335	1	TNR6_HUMAN
44	65.5	11.3	366	1	HOMI_MOUSE
45	65.5	11.3	724	1	PRTP_PRVIF

#### ALIGNMENTS

O63744 r rho-gtpas  
O9ck03 pasteurella  
O8uf01 agrobacteri  
O77736 sus scrofa  
P37060 vibrio chol  
O96q01 homo sapien  
O9qwn8 rattus norv  
P56960 mus musculu  
P48681 homo sapien  
P25445 homo sapien  
Q922Y3 mus musculu  
P11871 pseudorabie



RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  
RT expression of recombinant soluble TNF-binding protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92250049; PubMed=1315717;  
RA Fuchs P., Strehl S., Dworak M., Himmler A., Ambros P.F.;  
RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
RT localization to chromosome 12p13";  
RL Genomics 13:219-224(1992).  
RN [7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong E.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Heiton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [9]  
RP SEQUENCE OF 41-45.  
RX MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RT "Two tumor necrosis factor-binding proteins purified from human  
RT urine. Evidence for immunological cross-reactivity with cell surface  
RT tumor necrosis factor receptors";  
RL J. Biol. Chem. 265:1531-1536(1990).  
RN [10]  
RP INTERACTION WITH BAG4.  
RX MEDLINE=99115917; PubMed=9915703;  
RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;  
RT "Prevention of constitutive TNF receptor 1 signaling by silencer of  
RT death domains";  
RL Science 283:543-546(1999).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFR.  
RX MEDLINE=93258809; PubMed=8387891;  
RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,  
RA Broger C., Loetscher H., Lesslauer W.;  
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
RT beta complex: implications for TNF receptor activation";  
RL Cell 73:431-445(1993).  
RN [12]  
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
RX MEDLINE=97094982; PubMed=8939750;  
RA Naismith J.H., Devine I.Q., Khono H., Sprang S.R.;  
RT "Structures of the extracellular domain of the type I tumor necrosis  
RT factor receptor";  
RL Structure 4:1251-1262(1996).  
RN [13]  
RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.  
RX MEDLINE=99213501; PubMed=10199409;  
RA McDermott M.F., Aksentijevich I., Galon J., McDermott E.M.,  
RA Ogunkolade B.W., Centola M., Mansfield E., Gadina M., Karenko L.,  
RA Petterson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,  
RA Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,  
RA Schliming R., Kumarajewa T.R., Cooper S.M., Vella J.P., Amos C.I.,  
RA Mulley J., Quane K.A., Molloy M.G., Knaki A., Powell R.J.,  
RA Hitman G.A., O'Shea J., Kastner D.L.;  
RT "Germline mutations in the extracellular domains of the 55 kDa TNF  
RT receptor, TNFR1, define a family of dominantly inherited  
RT autoinflammatory syndromes";  
RL Cell 97:133-144(1999).  
RN [14]  
RP FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-  
CC specific cysteine proteases) mediating apoptosis. Contributes to  
CC the induction of noncytotoxic TNF effects including anti-viral  
CC state and activation of the acid sphingomyelinase.  
CC SUBUNIT: Binding of TNF to the extracellular domain leads to  
CC homotrimerization. The aggregated death domains provide a novel  
CC molecular interface that interacts specifically with the death  
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
CC RIP and possibly FADD, are recruited to the complex by their  
CC association with TRADD. This complex activates at least two  
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
CC Binds BAG4.  
CC SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
CC DOMAIN: The domain that induces A-SMASE is probably identical to  
CC the death domain. The N-SMASE activation domain (NSD) is both  
CC necessary and sufficient for activation of N-SMASE.  
CC PTM: The soluble form is produced from the membrane form by  
CC proteolytic processing.  
CC DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant  
CC familial hibernian fever (FHF) [MIM:142680]. FHF is a disease  
CC characterized by recurrent fever, abdominal pain, localized tender  
CC skin lesions and myalgia.  
CC SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC SIMILARITY: Contains 1 death domain.  
CC DATABASE: NAME=PRO; NOTE=CD guide CD120a entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm".  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X55313; CAA39021.1; -  
CC EMBL; M33294; AAA03210.1; -  
CC EMBL; M58286; AAA36753.1; -  
CC EMBL; M63121; AAA36754.1; -  
CC EMBL; M75866; AAA61201.1; -  
CC EMBL; M75864; AAA61201.1; JOINED.  
CC EMBL; M75865; AAA61201.1; JOINED.  
CC EMBL; M60275; AAA36756.1; -  
CC EMBL; A21522; CAA01558.1; -  
CC EMBL; AV13197; AAM77802.1; -  
CC EMBL; SC010140; AAH10140.1; -  
CC PIR; A38208; GQHUT1.  
CC PDB; 1TNR; 31-JUL-94.  
CC PDB; 1NCF; 07-DEC-95.  
CC PDB; 1EXT; 11-JAN-97.  
CC PDB; 1FT4; 12-OCT-01.  
CC PDB; 1ICH; 01-APR-02.  
CC Genew; HGNC:11916; TNFRSF1A.  
CC MIM; 191190; -  
CC MIM; 142680; -  
CC GO; GO:0005576; C:extracellular; TAS.  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0005032; P:tumor necrosis factor receptor cell differe. .; TAS.  
CC GO; GO:0007165; P:signal transduction; TAS.

Query Match 100.0%; Score 582; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 9e-54;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKQSLDTPATLYAVVNPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQY5ML 60  
Db 345 AHKQSLDTPATLYAVVNPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQY5ML 404

Qy 61 ATWRRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111  
Db 405 ATWRRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 2  
TRIA\_PIG STANDARD; PRT; 461 AA.  
AC P50555;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
DE (TNF-R1) (TNF-R1) (p55).  
GN TNFRSF1A OR TNFR1.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=96011645; PubMed=7590278;  
RA Suter B., Pauli U.H.;  
RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.";  
RL Gene 163:263-266(1995).

CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-  
CC specific cysteine proteases) mediating apoptosis (By similarity).  
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to  
CC homotrimerization. The aggregated cell domains provide a novel  
CC molecular interface that interacts specifically with the death  
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
CC RIP and possibly FADD, are recruited to the complex by their  
CC association with TRADD. This complex activates at least two  
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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CC EMBL; U19994; AAC48499.1; -.  
CC PIR; JC4302; JC4302.  
CC HSSP; P19438; 1TNR.  
CC InterPro; IPR000488; Death.  
CC InterPro; IPR001368; TNFR\_c6.  
CC Pfam; PF00531; death; 1.  
CC Pfam; PF00020; TNFR\_c6; 3.  
CC SMART; SM00005; DEATH; 1.  
CC SMART; SM00208; TNFR; 4.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
CC PROSITE; PS00652; TNFR\_NGFR\_2; 2.

DR PROSITE; PS0017; DEATH DOMAIN; 1.  
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR  
FT SUPERFAMILY MEMBER 1A.  
FT DOMAIN 22 210 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 211 233 POTENTIAL.  
FT DOMAIN 234 461 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 43 82 TNFR-CYS 1.  
FT REPEAT 83 125 TNFR-CYS 2.  
FT REPEAT 126 166 TNFR-CYS 3.  
FT REPEAT 167 195 TNFR-CYS 4.  
FT DOMAIN 340 350 N-SMASE ACTIVATION DOMAIN (NSD).  
FT DOMAIN 362 447 DEATH.  
FT DISULFID 44 58 BY SIMILARITY.  
FT DISULFID 59 72 BY SIMILARITY.  
FT DISULFID 62 81 BY SIMILARITY.  
FT DISULFID 84 99 BY SIMILARITY.  
FT DISULFID 102 117 BY SIMILARITY.  
FT DISULFID 105 125 BY SIMILARITY.  
FT DISULFID 127 143 BY SIMILARITY.  
FT DISULFID 146 158 BY SIMILARITY.  
FT DISULFID 149 166 BY SIMILARITY.  
FT DISULFID 168 179 BY SIMILARITY.  
FT DISULFID 182 194 BY SIMILARITY.  
FT DISULFID 185 190 BY SIMILARITY.  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 461 AA; 50696 MW; CD72361EC60C9D43 CRC64;

Query Match 79.5%; Score 462.5; DB 1; Length 461;  
Best Local Similarity 83.0%; Pred. No. 3.5e-41;  
Matches 93; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

Qy 1 AHK-POSLODTPATLYAVVNPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQY5M 59  
Db 350 AHSAPQLADADPATLYAVVNPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQY5M 409

Qy 60 LATWRRTPPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111  
Db 410 LAEWRRTPPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 461

RESULT 3  
TRIA\_BOVIN STANDARD; PRT; 471 AA.  
AC O19131;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
DE (TNF-R1) (TNF-R1) (p55).  
GN TNFRSF1A OR TNFR1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Aorta;  
RX MEDLINE=98271505; PubMed=9613449;  
RA Lee E.-K., Kehrl M.E. Jr., Taylor M.J.;  
RT "Cloning and sequencing of cDNA encoding bovine tumor necrosis factor  
RL (TNF)-receptor I.";  
RL Vet. Immunol. Immunopathol. 61:379-385(1998).  
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-  
CC specific cysteine proteases) mediating apoptosis (By similarity).  
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to  
CC homotrimerization. The aggregated cell domains provide a novel  
CC molecular interface that interacts specifically with the death  
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
CC RIP and possibly FADD, are recruited to the complex by their  
CC association with TRADD. This complex activates at least two  
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.

specific cysteine proteases) mediating apoptosis (By similarity).  
 -!- SUBUNIT: Binding of TNF to the extracellular domain leads to homotrimerization. The aggregated death domains provide a novel molecular interface that interacts specifically with the death domain of TRADD. Various TRADD-interacting proteins such as TRAFs, RIP and possibly FADD, are recruited to the complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NF-kappa-B signaling. Binds BAG4 (By similarity).  
 -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 -!- SIMILARITY: Contains 1 death domain.  
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 EMBL; U90937; AAB65143.1; -.  
 HSSP; P19438; 1TNR.  
 InterPro; IPR000488; Death.  
 InterPro; IPR001368; TNFR\_c6.  
 Pfam; PF00531; death; 1.  
 Pfam; PF00020; TNFR\_c6; 3.  
 SMART; SM00005; DEATH; 1.  
 SMART; SM00208; TNFR; 3.  
 PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
 PROSITE; PS00017; DEATH\_DOMAIN; 1.  
 Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 471  
 FT DOMAIN 22 210  
 FT TRANSMEM 211 233  
 FT DOMAIN 234 471  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 195  
 FT DOMAIN 340 360  
 FT DOMAIN 372 457  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 194  
 FT DISULFID 185 190  
 FT CARBOHYD 54 54  
 FT CARBOHYD 145 145  
 FT CARBOHYD 151 151  
 SQ SEQUENCE 471 AA; 51367 MW; 5243EF514DF81C4 CRC64;  
 Query Match 72.9%; Score 424; DB 1; Length 471;  
 Best Local Similarity 79.4%; Pred. No. 4.1e-37;  
 Matches 85; Conservative 5; Mismatches 17; Indels 0; Gaps 0;  
 QY 4 PQSLDTPATLYAVVENVPLRWKFEVRRRLGLSDHEIDRLQLNGRCLEAQSMLATW 63  
 DB 364 PDQLADADPATLYAVVGVGPPSRKVELVRLGLSEHEIERLENGRHLREAQYSMLAAW 423  
 QY 64 RRRTPREATLELGRVLRMDMLGCLIEDIEALCGPAALPAPSL 110  
 DB 424 RRRTPREATLELGRVLRMDMLGCLIEDIEALCGPAALPAPSL 110  
 DB 424 RRRTPREATLELGRVLRMDMLGCLIEDIEALCGPAALPAPSL 110  
 DB 424 RRRTPREATLELGRVLRMDMLGCLIEDIEALCGPAALPAPSL 110

## RESULT 4

TRIA RAT  
 ID TRIA RAT STANDARD; PRT; 461 AA.  
 AC P22934; Q91V30; Q91Y93;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1992 (Rel. 21, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
 DE (TNF-R1) (TNF-R1) (p55).  
 GN TNFRSF1A OR TNFR1 OR TNFR-1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91090841; PubMed=1702293;  
 RA Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K., Lantzi M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;  
 RT "Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.";  
 RL DNA Cell Biol. 9:705-715(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.  
 RC STRAIN=BB(DR)Wor, LEW/NHsd, ACI/SegHsd, DA/Bkl, F344/NHsd, and EN/SENHsd;  
 RA Furuya T., Salstrom J.L., Bina J., Hashimoto A., Dobbins D.E., Wilder R.L., Remmers E.F.;  
 RT "Polymorphisms of the tumor necrosis factor receptor type 1 locus among autoimmune susceptible and resistant inbred rat strains.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric TNFR1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis (By similarity).  
 CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to homotrimerization. The aggregated death domains provide a novel molecular interface that interacts specifically with the death domain of TRADD. Various TRADD-interacting proteins such as TRAFs, RIP and possibly FADD, are recruited to the complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NF-kappa-B signaling. Binds BAG4 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -!- SIMILARITY: Contains 1 death domain.  
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 EMBL; M63122; AAA42256.1; -.  
 EMBL; AF329976; AAK53562.1; -.  
 EMBL; AF329977; AAK53563.1; -.  
 EMBL; AF329981; AAK53567.1; -.  
 EMBL; AF329978; AAK53564.1; -.  
 EMBL; AF329979; AAK53565.1; -.  
 EMBL; AF329980; AAK53566.1; -.  
 PIR; B36555; GORTT1.  
 HSSP; P19438; 1NCF.  
 InterPro; IPR000488; Death.  
 InterPro; IPR001368; TNFR\_c6.  
 Pfam; PF00531; death; 1.  
 Pfam; PF00020; TNFR\_c6; 4.

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DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGRF_1; 3.
DR PROSITE; PS00652; TNFR_NGRF_2; 3.
DR PROSITE; PS00652; TNFR_NGRF_3; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 461
FT DOMAIN 22 211
FT TRANSMEM 212 234
FT REPEAT 235 461
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT DOMAIN 344 354
FT DOMAIN 363 448
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 195
FT DISULFID 185 191
FT CARBOHYD 54 54
FT CARBOHYD 151 151
FT CARBOHYD 201 201
FT VARIANT 230 230
FT VARIANT 295 295
FT VARIANT 344/450/451/452/453/454/455/456/457/458/459/460/461/462/463/464/465/466/467/468/469/470/471/472/473/474/475/476/477/478/479/480/481/482/483/484/485/486/487/488/489/490/491/492/493/494/495/496/497/498/499/500/501/502/503/504/505/506/507/508/509/510/511/512/513/514/515/516/517/518/519/520/521/522/523/524/525/526/527/528/529/530/531/532/533/534/535/536/537/538/539/540/541/542/543/544/545/546/547/548/549/550/551/552/553/554/555/556/557/558/559/560/561/562/563/564/565/566/567/568/569/570/571/572/573/574/575/576/577/578/579/580/581/582/583/584/585/586/587/588/589/590/591/592/593/594/595/596/597/598/599/600/601/602/603/604/605/606/607/608/609/610/611/612/613/614/615/616/617/618/619/620/621/622/623/624/625/626/627/628/629/630/631/632/633/634/635/636/637/638/639/640/641/642/643/644/645/646/647/648/649/650/651/652/653/654/655/656/657/658/659/660/661/662/663/664/665/666/667/668/669/670/671/672/673/674/675/676/677/678/679/680/681/682/683/684/685/686/687/688/689/690/691/692/693/694/695/696/697/698/699/700/701/702/703/704/705/706/707/708/709/710/711/712/713/714/715/716/717/718/719/720/721/722/723/724/725/726/727/728/729/730/731/732/733/734/735/736/737/738/739/740/741/742/743/744/745/746/747/748/749/750/751/752/753/754/755/756/757/758/759/760/761/762/763/764/765/766/767/768/769/770/771/772/773/774/775/776/777/778/779/780/781/782/783/784/785/786/787/788/789/790/791/792/793/794/795/796/797/798/799/800/801/802/803/804/805/806/807/808/809/810/811/812/813/814/815/816/817/818/819/820/821/822/823/824/825/826/827/828/829/830/831/832/833/834/835/836/837/838/839/840/841/842/843/844/845/846/847/848/849/850/851/852/853/854/855/856/857/858/859/860/861/862/863/864/865/866/867/868/869/870/871/872/873/874/875/876/877/878/879/880/881/882/883/884/885/886/887/888/889/890/891/892/893/894/895/896/897/898/899/900/901/902/903/904/905/906/907/908/909/910/911/912/913/914/915/916/917/918/919/920/921/922/923/924/925/926/927/928/929/930/931/932/933/934/935/936/937/938/939/940/941/942/943/944/945/946/947/948/949/950/951/952/953/954/955/956/957/958/959/960/961/962/963/964/965/966/967/968/969/970/971/972/973/974/975/976/977/978/979/980/981/982/983/984/985/986/987/988/989/990/991/992/993/994/995/996/997/998/999/1000/1001/1002/1003/1004/1005/1006/1007/1008/1009/1010/1011/1012/1013/1014/1015/1016/1017/1018/1019/1020/1021/1022/1023/1024/1025/1026/1027/1028/1029/1030/1031/1032/1033/1034/1035/1036/1037/1038/1039/1040/1041/1042/1043/1044/1045/1046/1047/1048/1049/1050/1051/1052/1053/1054/1055/1056/1057/1058/1059/1060/1061/1062/1063/1064/1065/1066/1067/1068/1069/1070/1071/1072/1073/1074/1075/1076/1077/1078/1079/1080/1081/1082/1083/1084/1085/1086/1087/1088/1089/1090/1091/1092/1093/1094/1095/1096/1097/1098/1099/1100/1101/1102/1103/1104/1105/1106/1107/1108/1109/1110/1111/1112/1113/1114/1115/1116/1117/1118/1119/1120/1121/1122/1123/1124/1125/1126/1127/1128/1129/1130/1131/1132/1133/1134/1135/1136/1137/1138/1139/1140/1141/1142/1143/1144/1145/1146/1147/1148/1149/1150/1151/1152/1153/1154/1155/1156/1157/1158/1159/1160/1161/1162/1163/1164/1165/1166/1167/1168/1169/1170/1171/1172/1173/1174/1175/1176/1177/1178/1179/1180/1181/1182/1183/1184/1185/1186/1187/1188/1189/1190/1191/1192/1193/1194/1195/1196/1197/1198/1199/1200/1201/1202/1203/1204/1205/1206/1207/1208/1209/1210/1211/1212/1213/1214/1215/1216/1217/1218/1219/1220/1221/1222/1223/1224/1225/1226/1227/1228/1229/1230/1231/1232/1233/1234/1235/1236/1237/1238/1239/1240/1241/1242/1243/1244/1245/1246/1247/1248/1249/1250/1251/1252/1253/1254/1255/1256/1257/1258/1259/1260/1261/1262/1263/1264/1265/1266/1267/1268/1269/1270/1271/1272/1273/1274/1275/1276/1277/1278/1279/1280/1281/1282/1283/1284/1285/1286/1287/1288/1289/1290/1291/1292/1293/1294/1295/1296/1297/1298/1299/1300/1301/1302/1303/1304/1305/1306/1307/1308/1309/1310/1311/1312/1313/1314/1315/1316/1317/1318/1319/1320/1321/1322/1323/1324/1325/1326/1327/1328/1329/1330/1331/1332/1333/1334/1335/1336/1337/1338/1339/1340/1341/1342/1343/1344/1345/1346/1347/1348/1349/1350/1351/1352/1353/1354/1355/1356/1357/1358/1359/1360/1361/1362/1363/1364/1365/1366/1367/1368/1369/1370/1371/1372/1373/1374/1375/1376/1377/1378/1379/1380/1381/1382/1383/1384/1385/1386/1387/1388/1389/1390/1391/1392/1393/1394/1395/1396/1397/1398/1399/1400/1401/1402/1403/1404/1405/1406/1407/1408/1409/1410/1411/1412/1413/1414/1415/1416/1417/1418/1419/1420/1421/1422/1423/1424/1425/1426/1427/1428/1429/1430/1431/1432/1433/1434/1435/1436/1437/1438/1439/1440/1441/1442/1443/1444/1445/1446/1447/1448/1449/1450/1451/1452/1453/1454/1455/1456/1457/1458/1459/1460/1461/1462/1463/1464/1465/1466/1467/1468/1469/1470/1471/1472/1473/1474/1475/1476/1477/1478/1479/1480/1481/1482/1483/1484/1485/1486/1487/1488/1489/1490/1491/1492/1493/1494/1495/1496/1497/1498/1499/1500/1501/1502/1503/1504/1505/1506/1507/1508/1509/1510/1511/1512/1513/1514/1515/1516/1517/1518/1519/1520/1521/1522/1523/1524/1525/1526/1527/1528/1529/1530/1531/1532/1533/1534/1535/1536/1537/1538/1539/1540/1541/1542/1543/1544/1545/1546/1547/1548/1549/1550/1551/1552/1553/1554/1555/1556/1557/1558/1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QY 6 SLDTDDPA-----TLXAVVENVPLRWKEFVRRLGLSDHIDRLQNGRCLE 54  
 DB 315 TISPSPASPMLOPGQLDMDVAVPARWKEFVRRLGLREAEIIEVEIGR-FRD 373  
 QY 55 AYSMLATWRRTPREATLEILGRVLRDMDLLGCLDIEEAL 97  
 DB 374 QQVEMLRWRQOQP---AGLGAVYAALERMGLDGCVEDLRSL 413

RESULT 7  
 T10B MOUSE STANDARD; PRT; 381 AA.  
 AC Q9QZM4; Q9JUL5; Q9JUL6;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (MK).  
 GN TNFRSF10B OR DR5 OR KILLER.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=99310501; PubMed=10383128;  
 RA Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.;  
 RT "Molecular cloning and functional analysis of the mouse homologue of the KILLER/DR5 tumor necrosis factor-related apoptosis-inducing ligand (TRAIL) death receptor.";  
 RL Cancer Res. 59:2770-2775(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Nakamura Y., Tamari M., Watanabe O.;  
 RT "Mouse TRAIL receptor.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Promotes the activation of NF-kappaB.  
 CC -!- SUBUNIT: Homotrimer. Can interact with TRADD and RIP (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Highly expressed in heart, lung and kidney.  
 CC -!- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.  
 CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 CC -!- SIMILARITY: Contains 1 death domain.

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EMBL; AF176833; AAD52656.1; -  
 DR EMBL; AB031081; BAA96462.1; -  
 DR EMBL; AB031082; BAA96463.1; -  
 DR HSSP; O14763; IDOG.  
 DR MGD; MGI:1341090; Tnfrsf10b.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death\_1\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 2.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 2.

DR PROSITE; PS00017; DEATH DOMAIN; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
 KW Receptor; Apoptosis; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 52 POTENTIAL.  
 FT CHAIN 53 381  
 FT DOMAIN 53 160 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 10B. EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 161 181 POTENTIAL.  
 FT DOMAIN 182 381 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 26 86 TNFR-CYS 1.  
 FT REPEAT 87 129 TNFR-CYS 2.  
 FT REPEAT 130 169 TNFR-CYS 3.  
 FT DOMAIN 273 356 DEATH.  
 FT DISULFID 74 85 BY SIMILARITY.  
 FT DISULFID 88 105 BY SIMILARITY.  
 FT DISULFID 108 121 BY SIMILARITY.  
 FT DISULFID 111 129 BY SIMILARITY.  
 FT DISULFID 131 145 BY SIMILARITY.  
 FT DISULFID 148 161 BY SIMILARITY.  
 FT DISULFID 151 169 BY SIMILARITY.  
 FT CONFLICT 42 42 M -> V (IN REF. 1).  
 FT CONFLICT 97 97 H -> R (IN REF. 2; BAA96463).  
 FT CONFLICT 128 128 V -> E (IN REF. 2; BAA96463).  
 FT CONFLICT 180 180 K -> N (IN REF. 2; BAA96463).  
 FT CONFLICT 187 187 L -> AT (IN REF. 2; BAA96463).  
 FT CONFLICT 215 215 R -> RAYP (IN REF. 2; BAA96463).  
 FT CONFLICT 229 229 L -> S (IN REF. 1).  
 FT CONFLICT 306 306 K -> R (IN REF. 2; BAA96463).  
 SQ SEQUENCE 381 AA; 42223 MW; 2F7999EA2EB485B1 CRC64;

Query Match 17.2%; Score 100; DB 1; Length 381;  
 Best Local Similarity 31.0%; Pred. No. 0.0044;  
 Matches 27; Conservative 14; Mismatches 34; Indels 12; Gaps 3;

QY 10 DDPATLYAVENVPL-RWKEFVRRLGLSDHIDRLQNGRCLEAQSMLATWRRTP 68  
 DB 270 DDLKFIIFYCSDIVFPDSWNRMLRQLGTDNQIKVKAET-LVTREALYQMLLKVRHQ- 327

QY 69 RREATLELLGRVLRDMDLLGCLDIEE 95  
 DB 328 -----GRSASINHLDDALEAVEE 345

RESULT 8  
 RIK1 HUMAN  
 ID RIK1 HUMAN STANDARD; PRT; 671 AA.  
 AC Q13546; Q13180;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Receptor-interacting serine/threonine protein kinase 2 (RC 2.7.1.37) (Serine/threonine protein kinase RIP) (Cell death protein RIP) (Receptor interacting protein).  
 DE (Receptor interacting protein).  
 GN RIK1 OR RIP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AUTOPHOSPHORYLATION, MUTAGENESIS OF LYS-45, AND INTERACTION WITH TRADD; TRAF1; TRAF2 AND TRAF3.  
 RC TISSUE=Umbilical vein endothelial cells;  
 RX MEDLINE=96200892; PubMed=8612133;  
 RA Hsu H., Huang J., Shu H.-B., Baichwal V.R., Goeddel D.V.;  
 RT "TNF-dependent recruitment of the protein kinase RIP to the TNF receptor-1 signaling complex.";  
 RL Immunity 4:387-396(1996).  
 RN [2]  
 RP REVISION TO 120.  
 RA Huang J., Hsu H., Baichwal V.R., Goeddel D.V.;  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]









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CC CC ENBL; U13616; AAA64834.1; --
CC CC PIR; A55575;
CC CC HSSP; P55273; IB18.
CC CC Genew; HGNC:494; ANK3.
CC CC MIM; 600465; --
CC CC GO; GO:0006605; P:protein targeting; NAS.
CC CC InterPro; IPR002110; ANK.
CC CC InterPro; IPR000488; Death.
CC CC Pfam; PF00023; ank; 24.
CC CC Pfam; PF00531; death; 1.
CC CC Pfam; PF00791; ZUS; 1.
CC CC PRINTS; PR01415; ANKYRIN.
CC CC SMART; SM00248; ANK; 21.
CC CC SMART; SM00005; DEATH; 1.
CC CC SMART; SM00218; ZUS; 1.
CC CC PROSITE; PS50088; ANK REPEAT; 21.
CC CC PROSITE; PS50297; ANK REP REGION; 1.
CC CC PROSITE; PS50017; DEATH DOMAIN; 1.
CC CC Cytoskeleton; Alternative splicing; Repeat; ANK repeat.
CC FT REPEAT 73 102 ANK 1.
CC FT REPEAT 106 135 ANK 2.
CC FT REPEAT 139 168 ANK 3.
CC FT REPEAT 172 201 ANK 4.
CC FT REPEAT 203 230 ANK 5.
CC FT REPEAT 234 263 ANK 6.
CC FT REPEAT 267 296 ANK 7.
CC FT REPEAT 300 329 ANK 8.
CC FT REPEAT 333 362 ANK 9.
CC FT REPEAT 366 395 ANK 10.
CC FT REPEAT 399 428 ANK 11.
CC FT REPEAT 432 461 ANK 12.
CC FT REPEAT 465 494 ANK 13.
CC FT REPEAT 498 527 ANK 14.
CC FT REPEAT 531 560 ANK 15.
CC FT REPEAT 564 593 ANK 16.
CC FT REPEAT 597 626 ANK 17.
CC FT REPEAT 630 659 ANK 18.
CC FT REPEAT 663 692 ANK 19.
CC FT REPEAT 696 725 ANK 20.
CC FT REPEAT 729 758 ANK 21.
CC FT REPEAT 762 791 ANK 22.
CC FT REPEAT 795 825 ANK 23.
CC FT DOMAIN 1519 1898 SER-RICH.
CC FT DOMAIN 4090 4174 DEATH.
CC SQ SEQUENCE 4377 AA; 480399 MW; F42379E55769B684 CRC64;

Query Match 13.8%; Score 80.5; DB 1; Length 4377;
Best Local Similarity 29.8%; Pred. No. 7.7;
Matches 25; Conservative 14; Mismatches 40; Indels 5; Gaps 2;

QY 17 AVVENPPLKWKFEVRLGLSDHEIDRLQLNGRCLEAQYSLATWRTPREATLEL 76
Db 4095 AIADHGLGLSWTELARELNPVSVEINQIRVENENSLISQSFMLKKKWT-R-DGKNATTDA 4153

QY 77 LGRVLRDMLLGLCIEIEEALCP 100
Db 4154 LTVSLTKINRI---DIVTLLEGP 4173

RESULT 12
ANK1_HUMAN
ID ANK1_HUMAN STANDARD; PRT; 1880 AA.
AC P16157;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ankyrin 1 (Erythrocyte ankyrin) (Ankyrin R).
GN ANK1 OR ANK.
OS Homo sapiens (Human).
```

```
OC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.; PARTIAL SEQUENCE, AND VARIANTS.
RC TISSUE=Hematopoietic;
RX MEDLINE=90158830; PubMed=2137557;
RA Lux S.E., John K.M., Bennett V.;
RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
RT structure with homology to tissue-differentiation and cell-cycle
RT control proteins.";
RL Nature 344:36-42(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90175370; PubMed=169849;
RA Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher D.,
RA Cheung M.C., Kan Y.W., Palek J.;
RT "cDNA sequence for human erythrocyte ankyrin.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
RN [3]
RP VARIANT HS ILB-462.
RX MEDLINE=96225450; PubMed=8640229;
RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tee W.T.,
RA Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
RT "Ankyrin-1 mutations are a major cause of dominant and recessive
RT hereditary spherocytosis.";
RL Nat. Genet. 13:214-218(1996).
CC -!- FUNCTION: Attach integral membrane proteins to cytoskeletal
CC elements; bind to the erythrocyte membrane protein band 4.2, to
CC Na-K ATPase, to the lymphocyte membrane protein GP85, and to the
CC cytoskeletal proteins fodrin, tubulin, vimentin and desmin.
CC Erythrocyte ankyrins also link spectrin (beta chain) to the
CC cytoplasmic domain of the erythrocytes anion exchange protein;
CC they retain most or all of these binding functions.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC PLASMA
CC MEMBRANE.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=2.1;
CC IsoId=P16157-1; Sequence=Displayed;
CC Name=2; Synonyms=2.2;
CC IsoId=P16157-2; Sequence=VSP_000264, VSP_000265;
CC Name=3;
CC IsoId=P16157-3; Sequence=VSP_000266;
CC -!- PTM: Regulated by phosphorylation.
CC -!- PTM: Palmitoylated.
CC -!- DISEASE: Defects in ANK1 are a cause of hereditary spherocytosis
CC (HS) [MIM:182900]. Inheritance can be autosomal dominant or
CC recessive.
CC -!- SIMILARITY: Contains 23 ANK repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC
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RESULT 12

ANK1\_HUMAN

ID ANK1\_HUMAN STANDARD; PRT; 1880 AA.

AC P16157;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Ankyrin 1 (Erythrocyte ankyrin) (Ankyrin R).

GN ANK1 OR ANK.

OS Homo sapiens (Human).

DR Pfam; PF00023; ank; 24.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00791; ZUS; 1.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR SMART; SM00248; ANK; 21.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00218; ZUS; 1.  
 DR PROSITE; PS50088; ANK REPEAT; 20.  
 DR PROSITE; PS50297; ANK REP REGION; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;  
 KW Phosphorylation; Lipoprotein; Disease mutation; Elliptocytosis;  
 KW Polymorphism.  
 FT INIT MET 0 0  
 FT DOMAIN 1 826  
 FT DOMAIN 827 1381  
 FT DOMAIN 1382 1880  
 FT REPEAT 43 72  
 FT REPEAT 76 105  
 FT REPEAT 109 138  
 FT REPEAT 142 171  
 FT REPEAT 173 200  
 FT REPEAT 204 233  
 FT REPEAT 237 266  
 FT REPEAT 270 299  
 FT REPEAT 303 332  
 FT REPEAT 336 365  
 FT REPEAT 369 398  
 FT REPEAT 402 431  
 FT REPEAT 435 464  
 FT REPEAT 468 497  
 FT REPEAT 501 530  
 FT REPEAT 534 563  
 FT REPEAT 567 596  
 FT REPEAT 600 629  
 FT REPEAT 633 662  
 FT REPEAT 666 695  
 FT REPEAT 699 728  
 FT REPEAT 732 761  
 FT REPEAT 765 794  
 FT DOMAIN 1402 1486  
 FT VARSPLIC 1512 1873  
 FT VARSPLIC 1874 1874  
 FT VARSPLIC 1849 1880  
 FT VARIANT 20 20  
 FT VARIANT 462 462  
 FT VARIANT 618 618  
 FT VARIANT 749 749  
 FT VARIANT 844 844  
 FT VARIANT 1285 1285  
 FT VARIANT 1391 1391  
 FT VARIANT 1591 1591  
 FT VARIANT 1698 1698  
 FT CONFLICT 229 229  
 FT CONFLICT 1545 1545  
 FT SEQUENCE 1880 AA; 206145 MW; 1C5F5E7EFD1CD428 CRC64;

99 kDa DOMAIN  
 (ANTION EXCHANGE PROTEIN BINDING DOMAIN).  
 62 kDa DOMAIN (SPECTRIN BINDING DOMAIN).  
 55 kDa REGULATORY DOMAIN  
 (REGULATES THE BINDING OF ANKYRIN TO  
 SPECTRIN AND THE BAND 3 PROTEIN).  
 ANK 1.  
 ANK 2.  
 ANK 3.  
 ANK 4.  
 ANK 5.  
 ANK 6.  
 ANK 7.  
 ANK 8.  
 ANK 9.  
 ANK 10.  
 ANK 11.  
 ANK 12.  
 ANK 13.  
 ANK 14.  
 ANK 15.  
 ANK 16.  
 ANK 17.  
 ANK 18.  
 ANK 19.  
 ANK 20.  
 ANK 21.  
 ANK 22.  
 ANK 23.  
 Missing (in isoform 2).  
 /FTid=VSP\_000264.  
 H -> D (in isoform 2).  
 /FTid=VSP\_000265.  
 TVEGLEDPSELEVDIDYFMKHSKDHSTPNP -> ELRGS  
 GLOPLDIEGRKGAQIVKRLKRGKQ (in isoform  
 3).  
 /FTid=VSP\_000266.  
 R -> T.  
 /FTid=VAR\_000595.  
 V -> I (in HS).  
 /FTid=VAR\_000596.  
 R -> H (in Brueggen).  
 /FTid=VAR\_000597.  
 V -> A.  
 /FTid=VAR\_000598.  
 D -> E.  
 /FTid=VAR\_000599.  
 E -> D.  
 /FTid=VAR\_000601.  
 S -> T.  
 /FTid=VAR\_000600.  
 D -> N (in Duesseldorf).  
 /FTid=VAR\_000602.  
 R -> D.  
 /FTid=VAR\_000603.  
 A -> S (in REF. 2).  
 V -> I (in REF. 2).  
 1880 AA; 206145 MW; 1C5F5E7EFD1CD428 CRC64;

Query Match 13.7%; Score 80; DB 1; Length 1880;  
 Best Local Similarity 30.1%; Pred. No. 3.4;  
 Matches 25; Conservative 14; Mismatches 42; Indels 2; Gaps 2;  
 QY 4 PQSLDTDDPATL-YAVVENVPFLRWKEFVRRLGLSDHEIDRLGLNGRCLREAOYSMLAT 62  
 DB 1393 PGSLSGTQAEKMAVISEHGLSWAELARELQSVEDINRVENPNSLLEQSVALLNL 1452  
 QY 63 WRRTPPREATLELLGRVLRDMD 85  
 DB 1453 WVIR-EGQNNANMENLYTALQSID 1474

RESULT 13  
 STILL SCHPO  
 ID ST11 SCHPO STANDARD; PRT; 591 AA.  
 AC Q9USI5; O13458;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Heat shock protein still homolog.  
 GN ST11 OR ST11 OR SPC645.14C.  
 OS Schizosaccharomyces pombe (Fission Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yamashita Y., Nakaseko Y., Samejima I., Kumada K., Yamada H.,  
 RA Yanagida M.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,  
 RA Welter J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Rhode G.,  
 RA Dega R.K., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McComb W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Bartell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880(2002).  
 CC -!- FUNCTION: MAY PLAY A ROLE IN MEDIATING THE HEAT SHOCK RESPONSE  
 CC OF SOME HSP70 GENES (BY SIMILARITY).  
 CC -!- SUBUNIT: PART OF A LARGER COMPLEX THAT INCLUDES HSP70, HSP90, AND  
 CC IMMUNOPHILINS (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Contains 9 TPR repeats.  
 CC -----  
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-----  
 ENBL; D85197; BAA22619.1; --  
 ENBL; AL049498; CAB39910.1; --  
 DR PIR; T41531.  
 DR PIR; T51996; T51996.  
 DR HSSP; P53041; 1A17.  
 DR GeneDB SPombe; SPCC645.14C; --  
 DR InterPro; IPR006636; STII; --  
 DR InterPro; IPR008941; TPR-like.  
 DR InterPro; IPR001440; TPR.  
 DR Pfam; PF00515; TPR; 8.  
 DR SMART; SMO0028; TPR; 8.  
 DR SMART; SMO0028; STII; 2.  
 DR SMART; SMO0028; TPR; 8.  
 KW Heat shock; TPR repeat; Repeat.  
 FT REPEAT 2 35  
 FT REPEAT 37 69 TPR 1.  
 FT REPEAT 70 103 TPR 2.  
 FT REPEAT 265 298 TPR 3.  
 FT REPEAT 299 331 TPR 4.  
 FT REPEAT 339 372 TPR 5.  
 FT REPEAT 399 432 TPR 6.  
 FT REPEAT 434 466 TPR 7.  
 FT REPEAT 467 500 TPR 8.  
 FT REPEAT 467 500 TPR 9.  
 FT CONFLICT 28 28 A -> T (IN REF. 1).  
 SQ SEQUENCE 591 AA; 65544 MW; D218FCDD5884B4AA CRC64;

Query Match 13.3%; Score 77.5; DB 1; Length 591;  
 Best Local Similarity 32.4%; Pred. No. 1.7;  
 Matches 24; Conservative 14; Mismatches 25; Indels 11; Gaps 3;  
 QY 40 EIDRLQLNGRCLEAQAQ-----YSMLATRRRTTPREATLELLGVLRLMDLGGCLEL- 92  
 Db 495 EVDREPTNGKRLREIESQLSKCMSASOR-----QNETEETWARIQKDEPVLIGLQDP 550  
 QY 93 IEALCGPAALPPA 106  
 Db 551 AMQAAILGQARENPA 564

RESULT 14  
 T10B\_HUMAN  
 ID T10B\_HUMAN STANDARD; PRT; 440 AA.  
 AC 014763; 015508; 015517; 015531; Q9BVE0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL receptor-2) (TRAIL-R2).  
 DE receptor-2) (TRAIL-R2).  
 GN TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF N-TERMINUS.  
 RC TISSUE=Foreskin fibroblast;  
 RX MEDLINE=97459925; PubMed=9311998;  
 RA Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y., Boiani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A., Goodwin R.G., Rauch C.T.;  
 RA "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";  
 RT EMBO J. 16:5386-5397(1997).  
 RL [2]  
 RN SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), ALTERNATIVE SPLICING, AND VARIANTS LEU-32 AND VAL-67.  
 RP SPLICING, AND VARIANTS LEU-32 AND VAL-67.  
 RX MEDLINE=97431692; PubMed=9285725;  
 RA Screaton G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E., McMichael A.J., Bell J.I.;

RT "TRICK2, a new alternatively spliced receptor that transduces the cytotoxic signal from TRAIL.";  
 RL Curr. Biol. 7:693-696(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), CHARACTERIZATION, AND VARIANTS LEU-32 AND VAL-67.  
 RP LEU-32 AND VAL-67.  
 RC TISSUE=Liver, and Spleen;  
 RX MEDLINE=98039016; PubMed=9373179;  
 RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N., Tschoopp J.;  
 RA "Characterization of two receptors for TRAIL.";  
 RT FEBS Lett. 416:329-334(1997).  
 RL [4]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RC TISSUE=Ovary;  
 RX MEDLINE=97467719; PubMed=9326928;  
 RA Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., Meng R., Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R., Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;  
 RA "KILLER/DR5 is a DNA damage-inducible p53-regulated death receptor gene.";  
 RT Nat. Genet. 17:141-143(1997).  
 RL [5]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RX MEDLINE=97390508; PubMed=9242610;  
 RA Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;  
 RA "An antagonist decoy receptor and a death domain-containing receptor for TRAIL.";  
 RT Science 277:815-818(1997).  
 RL [6]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.  
 RX MEDLINE=97467318; PubMed=9325248;  
 RA MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T., Cohen G.M., Alnemri E.S.;  
 RA "Identification and molecular cloning of two novel receptors for the cytotoxic ligand TRAIL.";  
 RT J. Biol. Chem. 272:25417-25420(1997).  
 RL [7]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.  
 RX MEDLINE=98090092; PubMed=9430227;  
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
 RT "Death receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
 RL Immunity 7:821-830(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANT LEU-32.  
 RX MEDLINE=97390509; PubMed=9242611;  
 RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M., Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I., Goddard A.D., Godowski P., Ashkenazi A.;  
 RA "Control of TRAIL-induced apoptosis by a family of signaling and decoy receptors.";  
 RT Science 277:818-821(1997).  
 RL [9]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANTS LEU-32 AND VAL-67.  
 RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;  
 RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2 gene in colorectal carcinoma.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RC Cao X., Zhang W., Wan T.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.  
 RA Farrah T., Vu T., Gilbert T., Gross J., O'Hara P.;  
 RT "Homo sapiens homolog of tumor necrosis factor receptor.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT LEU-32.  
 RC TISSUE=Cervix;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,



RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP INTERACTION WITH PEAL5.  
 RX MEDLINE=99369240; PubMed=10442631;  
 RA Condorelli G., Vigliotta G., Cafieri A., Trencia A., Andalo P.,  
 RA Oriente F., Miele C., Caruso M., Formisano P., Beguinot F.,  
 RT "PED/PEA-15: an anti-apoptotic molecule that regulates FAS/TNFR1-  
 RT induced apoptosis";  
 RL Oncogene 18:4409-4415(1999).  
 RN [5]  
 RP STRUCTURE BY NMR OF 1-83.  
 RX MEDLINE=98241233; PubMed=9582077;  
 RA Eberstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,  
 RA Leonardo M.J., Fesik S.W.,  
 RT "NMR structure and mutagenesis of the FADD (Mort1) death-effector  
 RT domain";  
 RL Nature 392:941-945(1998).  
 CC -!- FUNCTION: Apoptotic adaptor molecule that recruits caspase-8 or  
 CC caspase-10 to the activated Fas (CD95) or TNFR-1 receptors. The  
 CC resulting aggregate called the death-inducing signaling complex  
 CC (DISC) performs caspase-8 proteolytic activation. Active caspase-8  
 CC initiates the subsequent cascade of caspases (aspartate-specific  
 CC cysteine proteases), mediating apoptosis.  
 CC -!- SUBUNIT: Interacts with CFLAR and PEAL5.  
 CC -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues, except  
 CC for peripheral blood mononuclear leukocytes.  
 CC -!- DOMAIN: Contains a death domain involved in the binding of the  
 CC corresponding domain within Fas receptor.  
 CC -!- SIMILARITY: Contains 1 death effector (DED) domain.  
 CC -!- SIMILARITY: Contains 1 death domain.  
 CC -----  
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 CC -----  
 DR EMBL: U24231; AAA86517.1; --  
 DR EMBL: X84703; CAAS9197.1; --  
 DR EMBL: BC000334; AAH00334.1; --  
 DR PIR: A56912; A56912.  
 DR PDB: 1A1W; 16-FEB-99.  
 DR PDB: 1A1Z; 16-FEB-99.  
 DR PDB: 1E3Y; 06-NOV-00.  
 DR PDB: 1E41; 06-NOV-00.  
 DR Genew: HGNC:3573; FADD.  
 DR MIM: 602457; --  
 DR GO: GO:0005039; F:death receptor-associated factor activity; TAS.  
 DR GO: GO:0008625; P:induction of apoptosis via death domain rec. . .; TAS.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001875; DED.

DR Pfam: PF00531; death; 1.  
 DR Pfam: PF01335; DED; 1.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00031; DED; 1.  
 DR PROSITE: PS50017; DEATH DOMAIN; 1.  
 DR PROSITE: PS0168; DED; 1.  
 KW Apoptosis; 3D-structure.  
 FT DOMAIN 3 81  
 FT DED.  
 FT DEDATH.  
 FT MUTAGEN 121 121  
 FT CONFLICT 32 32  
 FT HELIX 3 28  
 FT TURN 29 31  
 FT HELIX 33 38  
 FT HELIX 42 52  
 FT TURN 53 53  
 FT TURN 57 58  
 FT TURN 61 70  
 FT HELIX 71 71  
 FT HELIX 73 81  
 SQ SEQUENCE 208 AA; 23279 MW; 0E65E2F852E83507 CRC64;  
 Query Match 12.8%; Score 74.5; DB 1; Length 208;  
 Best Local Similarity 29.9%; Pred. NO. 1.1;  
 Matches 26; Conservative 18; Mismatches 38; Indels 5; Gaps 4;  
 QY 13 ATLYAVENVPLRWKEFVRRGLSDHEIDRLQLNGRCLEAQYSLATWRRTPREA 72  
 DB 99 AAFNVICDNVKG-DWRRLARQLKVSITKIDSDIEDRYRNLTFRVRESLRW-KNTSENA 156  
 QY 73 TLELLGRVLR--DMDLGLCL-EDIEEA 96  
 DB 157 TWAHLVGLRSCQNNLVADLVQEVQQA 183  
 Search completed: June 1, 2004, 14:44:29  
 Job time : 8.97605 secs

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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:35:21 ; Search time 33.2335 Seconds  
(without alignments)  
1053.831 Million cell updates/sec

Title: US-09-854-906-8

Perfect score: 582

Sequence: 1 AKPQSLDTPATLYAVVE.....DIEALCGPAALPPAPSLLR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477.5	82.0	446	Q95ND3	Q95nd3 felis silve
2	158	27.1	387	Q8VD70	Q8vd70 mus musculu
3	152	26.1	413	Q99MM1	Q99mm1 mus musculu
4	86	14.8	1848	Q1302	Q1302 mus musculu
5	83.5	14.3	368	Q57408	Q57408 melesgris g
6	83	14.3	273	Q9V8H5	Q9v8h5 drosophila
7	83	14.3	410	Q7T3M8	Q7t3m8 gallus gall
8	82.5	14.2	365	Q81645	Q81645 hepatitis c
9	82.5	14.2	3011	Q913D4	Q913d4 hepatitis c
10	82	14.1	163	Q9YB1	Q9ybb1 aeropyrum p
11	81.5	14.0	364	Q68797	Q68797 hepatitis c
12	81.5	14.0	365	Q81652	Q81652 hepatitis c
13	81.5	14.0	3011	Q81754	Q81754 hepatitis c
14	81.5	14.0	3022	Q68798	Q68798 hepatitis c
15	81	13.9	626	Q9KXP5	Q9kxp5 streptomyce
16	80.5	13.8	143	O70510	O70510 rattus norv

17	80.5	13.8	314	6	Q861W6	Q861w6 felis silve
18	80.5	13.8	838	11	Q9QXH1	Q9qxh1 mus musculu
19	80.5	13.8	960	11	Q8VDA0	Q8vda0 rattus norv
20	80.5	13.8	1093	11	Q8CBN3	Q8cbn3 mus musculu
21	80.5	13.8	1726	11	Q8VC68	Q8vc68 mus musculu
22	80.5	13.8	1762	11	O88521	O88521 rattus norv
23	80.5	13.8	1887	4	Q7Z3G4	Q7z3g4 homo sapien
24	80.5	13.8	1943	11	O61307	O61307 mus musculu
25	80.5	13.8	2622	11	O70511	O70511 rattus norv
26	80	13.7	1038	11	Q80ZZ7	Q80zz7 mus musculu
27	80	13.7	1050	11	Q8CCV0	Q8ccv0 mus musculu
28	80	13.7	1719	4	Q13768	Q13768 homo sapien
29	80	13.7	1856	4	Q99407	Q99407 homo sapien
30	79	13.6	303	5	Q9NHG0	Q9nhg0 drosophila
31	79	13.6	965	4	Q7Z344	Q7z344 homo sapien
32	79	13.6	1863	4	Q7Z3L5	Q7z3l5 homo sapien
33	78.5	13.5	319	6	Q9TV79	Q9tv79 oryctolagus
34	78.5	13.5	320	6	Q9XS29	Q9xs29 oryctolagus
35	78.5	13.5	388	16	Q97PS5	Q97ps5 streptococ
36	78.5	13.5	634	5	Q8STZ1	Q8stz1 encephalito
37	78.5	13.5	811	4	Q9HQP5	Q9hqp5 homo sapien
38	77.5	13.3	356	10	Q8GRN3	Q8grn3 oryza sativ
39	77	13.2	202	13	Q9DEY7	Q9dey7 poephila gu
40	77	13.2	316	16	Q9HXZ2	Q9hxz2 pseudomonas
41	76.5	13.1	205	4	Q742I8	Q742i8 homo sapien
42	76.5	13.1	364	12	Q68824	Q68824 hepatitis c
43	76.5	13.1	364	12	Q68805	Q68805 hepatitis c
44	76.5	13.1	634	5	Q8ST44	Q8st44 encephalito
45	75.5	13.0	364	12	Q92543	Q92543 hepatitis c

## ALIGNMENTS

RESULT 1

Q95ND3 PRELIMINARY; PRT; 446 AA.  
AC Q95ND3;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Tumor necrosis factor type I.  
GN TNFR I.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;  
RT "Molecular cloning of feline tumor necrosis factor receptor type I  
RT (TNFR I) and expression of TNFR I and TNFR II in various disease in  
RT cats.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB051103; BAB5455.1; -  
DR GO; GO:0005489; F:electron transporter activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0006118; P:electron transduction; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR006209; EGF like.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00190; CYTOCHROME C; 1.  
DR PROSITE; PS0017; DEATH DOMAIN; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
SQ SEQUENCE 446 AA; 49563 MW; 217BD331DD8A74AA CRC64;



```

Query Match      82.0%; Score 477.5; DB 6; Length 446;
Best Local Similarity 84.4%; Pred. No. 2.6e-42;
Matches 92; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 3 KPSLTDTPATYAYVENVPPRWKEFVRRLGSLDHEIDRLQNGRCLEAQQYSLMAT 62
Db 339 RPEA-DPATYAYVVDGVFPFGRWKEFVRRLGSLDHEIDRLQNGRCLEAQQYSLMAT 397

QY 63 WRRRTPREATLELLGVRLDMDLGLCLEDIEEALCPAALPAPSLR 111
Db 398 WRRRTPREATLELLGVRLDMDLGLCLEDIEEALCPAALPAPSLR 446

RESULT 2
Q8VD70 PRELIMINARY; PRT; 387 AA.
AC Q8VD70;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 12.
GN TNFRSF25 OR TNFRSF12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017526; AAI17526.1; -.
DR MGD; MGI:1934667; Tnfrsf25.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR SMART; SM00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 387 AA; 41640 MW; F16644666BAD68D3 CRC64;

Query Match      27.1%; Score 158; DB 11; Length 387;
Best Local Similarity 44.6%; Pred. No. 1.9e-08;
Matches 37; Conservative 12; Mismatches 30; Indels 4; Gaps 2;

QY 15 LYAVENVPPLRWKEFVRRLGSLDHEIDRLQNGRCLEAQQYSLMATWRRRTPREATL 74
Db 305 LYDVMDDAVPARRWKEFVRTGLREAEIAEVEICR-FRDQQYEMLKRWQQQP---AGL 360

QY 75 ELGLGVRLDMDLGLCLEDIEEAL 97
Db 361 GAIYAALERKLGEGCAEDLSRL 383

RESULT 3
Q99MM1 PRELIMINARY; PRT; 413 AA.
AC Q99MM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE WSL-1-like protein.
GN TNFRSF25 OR TNFRSF12.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RC SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=21158384; PubMed=11261933;
RX Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
RA Owen M.J.;
RT "Genomic structure, expression, and chromosome mapping of the mouse
RT homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)
RT gene.";
RL Immunogenetics 53:59-63(2001).
DR EMBL; AF329969; AAK11256.1; -.
DR HSSP; Q92956; IJMA.
DR MGD; MGI:1934667; Tnfrsf25.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 413 AA; 44453 MW; 69F21B85DDDBABF CRC64;

Query Match      26.1%; Score 152; DB 11; Length 413;
Best Local Similarity 43.4%; Pred. No. 8.8e-08;
Matches 36; Conservative 12; Mismatches 31; Indels 4; Gaps 2;

QY 15 LYAVENVPPLRWKEFVRRLGSLDHEIDRLQNGRCLEAQQYSLMATWRRRTPREATL 74
Db 331 LYDVMDDAVPARRWKEFVRTGLREAEIAEVEICR-FRDQQYEMLKRWQQQP---AGL 386

QY 75 ELGLGVRLDMDLGLCLEDIEEAL 97
Db 387 GAIYAALERKLGEGCAEDLSRL 409

RESULT 4
Q61302 PRELIMINARY; PRT; 1848 AA.
AC Q61302;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Erythroid ankyrin.
GN ANK1 OR ANK-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Nervous system;
RX MEDLINE=93252825; PubMed=8486643;
RX Birkenmeier C.S., White R.A., Peters L.L., Hall E.J., Lux S.E.,
RA Barker J.E.;
RT "Complex patterns of sequence variation and multiple 5' and 3' ends
RT are found among transcripts of the erythroid ankyrin gene.";
RL J. Biol. Chem. 268:9533-9540(1993).
DR EMBL; X69063; CAA4801.1; -.
DR PIR; S3771; S3771.
DR HSSP; Q00420; 1AWC.
DR MGD; MGI:88024; Ank1.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.

```



```
[2]
RN  SEQUENCE FROM N.A.
RC  STRAIN=Berkeley;
RA  Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., George R.,
RA  Champe M., Chavez C., Dorsett V., Farfan D., Friese E., George R.,
RA  Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA  Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA  Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL  Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AE003799; AAF57692.1; -
DR  EMBL; AY051558; AAK92982.1; -
DR  FlyBase; FBgn0013983; imd.
DR  GO; GO:0006961; P:antibacterial humoral response (sensu Inver. . .; IMP.
DR  GO; GO:0006963; P:antibacterial polypeptide induction; IMP.
DR  GO; GO:0006959; P:humoral immune response; IMP.
DR  InterPro; IPR000488; Death.
DR  Pfam; PF00531; death; 1.
DR  PROSITE; PS00017; DEATH DOMAIN; 1.
SQ  SEQUENCE 273 AA; 29899 MW; 7247CA4B46F5545B CRC64;

Query Match 14.3%; Score 83; DB 5; Length 273;
Best Local Similarity 24.8%; Pred. No. 1-2;
Matches 26; Conservative 25; Mismatches 38; Indels 16; Gaps 3;

QY 3 KPQSLDTPDPAITYAVVEN--VPPLR-----WKFFVRLGLSDHEIDR--LEL 46
DB 153 KPRASATRTXSVIAMWQSQEPDVLDDVSTHGLGKGNQVNRDLGMSEGQIDQAIIDH 212
QY 47 QNGRCLEAQYSMLATRRRTPREATLELGLVLRDMDLLGCLG 91
DB 213 QMGNIREVIYQLLQWIRSSADGVAIVGLRTLLWESQRDCVQ 257

RESULT 7
QY7T3M8 PRELIMINARY; PRT; 410 AA.
AC QY7T3M8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Death domain-containing tumor necrosis factor receptor superfamily
DE member 23 variant 1 (Fragment).
OS Gallus Gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Identification and characterization of alternatively spliced, ovarian
RT enhanced death receptor and decoy receptor.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251408; AAP41833.1; -
KW Receptor.
FT NON TER 410
SQ SEQUENCE 410 AA; 46194 MW; 4BFC7C7016C2BA60 CRC64;

Query Match 14.3%; Score 83; DB 13; Length 410;
Best Local Similarity 25.7%; Pred. No. 1.9;
Matches 18; Conservative 21; Mismatches 29; Indels 2; Gaps 2;

QY 16 YAVVENVPLRWKFFVRLGLSDHEIDRLQNGRCLEAQYSMLATRRRTPREATLE 75
DB 325 PAFIKVPPVKWRKLM-RTHLEENDIDKIIYNWPNIDDEQSQMLLMWKNKQKQSIK 383
QY 76 ILGRVLRDMD 85
DB 384 LLDE-LWDID 392

RESULT 8
QY81645
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QY81645 PRELIMINARY; PRT; 365 AA.
AC QY81645;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NS5 (Genome polypeptide) (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS117;
RX MEDLINE=94172337; PubMed=8126459;
RA Okamoto H., Kojima M., Sakamoto M., Iizuka H., Hadiwandono S.,
RA Suwignyo S., Miyakawa Y., Mayumi M.;
RT "The entire nucleotide sequence and classification of a hepatitis C
RT virus isolate of a novel genotype from an Indonesian patient with
RT chronic liver disease.";
RL J. Gen. Virol. 75:629-635 (1994).
DR EMBL; D16190; BAA03731.1; -
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:virial genome replication; IEA.
DR InterPro; IPR002166; HCV_RGRP.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF00998; Viral_RGRP; 1.
KW Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;
KW Transferase.
FT NON TER 1
SQ SEQUENCE 365 AA; 40296 MW; B5DAD6519868B630 CRC64;

Query Match 14.2%; Score 82.5; DB 12; Length 365;
Best Local Similarity 27.8%; Pred. No. 1.9;
Matches 35; Conservative 12; Mismatches 38; Indels 41; Gaps 6;

QY 2 HKPQSLDTPDPAITYAVVENVPLRWKFFVRL-GL-----SDHEIDRLQNGRC 52
DB 212 HLEKALDCE---IYCAVHSVQPLDPEIQRLHGLSAFSLHSYSPGEINRV---AAC 263
QY 53 REAQYSMLATRRRTPREATLELGLVLRDMDLLGCLDEHEALCG-----PAA 102
DB 264 RKLGVPLRWRHRARSVRATLLSQGG-----KAAICGKYLFWNAVTKLIK 309
QY 103 LPPAPS 108
DB 310 LTFPLPS 315

RESULT 9
QY913D4 PRELIMINARY; PRT; 3011 AA.
AC QY913D4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Genome polypeptide.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Guntaka R.V., Mupally S.K., Khaja M.N., Kota K.K., Ramana V.K.,
RA Swaminathan S., Sakata Y., Habeebullah C.M.;
RT "Nucleotide Sequence of Indian strain of Hepatitis C Virus.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS;
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DR GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
DR GO:0016740; F:transferase activity; IEA.  
DR GO:0006350; P:transcription; IEA.  
DR GO:0019079; P:viral genome replication; IEA.  
DR InterPro; IPR002166; HCV\_RdRP.  
DR InterPro; IPR007094; RNA\_pol\_PSVir.  
KW Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;  
KW Transferase.  
FT NON\_TER  
SQ SEQUENCE 364 AA; 40406 MW; AD01ACDF4F73D95E CRC64;  
  
Query Match 14.0%; Score 81.5; DB 12; Length 364;  
Best Local Similarity 28.0%; Pred. No. 2.4;  
Matches 30; Conservative 12; Mismatches 32; Indels 33; Gaps 5;  
  
QY 2 HKPQSLDTPATLYAVVENVPLRWKFEVRL-----CLSDHEIDRLQLNGRCL 52  
DB 213 HK--ALDFD---MYGVNTITPLDLPQIIQRLHGMASFSLHSGYSGELNRV----GACL 262  
QY 53 REAQYSLMATWRRTTREPATELLGRVLRDMDLLGCLLEIDIEALCG 99  
DB 263 RKLGVPLPRAWHRARAVRAKLIQSG-----KAAICG 295  
  
RESULT 12  
Q81652 PRELIMINARY; PRT; 365 AA.  
ID Q81652  
AC Q81652  
DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
DE NS5 (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HC-G9;  
RA Okamoto H.;  
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HC-G9;  
RX MEDLINE=94172337; PubMed=8126459;  
RA Okamoto H., Kojima M., Sakamoto M., Iizuka H., Hadiwandowo S.,  
Suwignyo S., Miyakawa Y., Mayumi M.;  
RT "The entire nucleotide sequence and classification of a hepatitis C  
RT virus isolate of a novel genotype from an Indonesian patient with  
RT chronic liver disease."  
RL J. Gen. Virol. 75:629-635 (1994).  
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
CC PROTEIN C AND RNA (BY SIMILARITY).  
DR EMBL; D14853; BAA03581.1; -  
DR PIR; P00804; P00804.  
DR HSP; P26663; IJXP.  
DR MEROPS; S29.001; -  
DR GO:0005524; F:ATP binding; IEA.  
DR GO:0008026; F:ATP dependent helicase activity; IEA.  
DR GO:0003723; F:RNA binding; IEA.  
DR GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
DR GO:0008236; F:serine-type peptidase activity; IEA.  
DR GO:0005198; F:structural molecule activity; IEA.  
DR GO:0016740; F:transferase activity; IEA.  
DR GO:0006350; P:transcription; IEA.  
DR GO:0019079; P:viral genome replication; IEA.  
DR InterPro; IPR007094; RNA\_pol\_PSVir.  
KW Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;  
KW Transferase.  
FT NON\_TER  
SQ SEQUENCE 365 AA; 40368 MW; EE7DF9DBC4186B9 CRC64;  
  
Query Match 14.0%; Score 81.5; DB 12; Length 365;  
Best Local Similarity 27.0%; Pred. No. 2.4;  
Matches 34; Conservative 13; Mismatches 38; Indels 41; Gaps 6;  
  
QY 2 HKPQSLDTPATLYAVVENVPLRWKFEVRL-GL-----SDHEIDRLQLNGRCL 52  
DB 212 HLEALDCE---IYCAVHSIQFLDLPETIIQRLHGLSAPLSHSYSGELNRV----AAAL 263  
QY 53 REAQYSLMATWRRTTREPATELLGRVLRDMDLLGCLLEIDIEALCG-----PAA 102

DB 264 RKLGVPLPRAWHRARAVRAKLIQSG-----KAAICGKYLFWAVKTLK 309  
QY 103 LPPAPS 108  
DB 310 LTPLES 315  
  
RESULT 13  
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ID Q81754  
AC Q81754  
DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
DE Genome polyprotein.  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HC-G9;  
RA Okamoto H.;  
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HC-G9;  
RX MEDLINE=94172337; PubMed=8126459;  
RA Okamoto H., Kojima M., Sakamoto M., Iizuka H., Hadiwandowo S.,  
Suwignyo S., Miyakawa Y., Mayumi M.;  
RT "The entire nucleotide sequence and classification of a hepatitis C  
RT virus isolate of a novel genotype from an Indonesian patient with  
RT chronic liver disease."  
RL J. Gen. Virol. 75:629-635 (1994).  
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
CC PROTEIN C AND RNA (BY SIMILARITY).  
DR EMBL; D14853; BAA03581.1; -  
DR PIR; P00804; P00804.  
DR HSP; P26663; IJXP.  
DR MEROPS; S29.001; -  
DR GO:0005524; F:ATP binding; IEA.  
DR GO:0008026; F:ATP dependent helicase activity; IEA.  
DR GO:0003723; F:RNA binding; IEA.  
DR GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
DR GO:0008236; F:serine-type peptidase activity; IEA.  
DR GO:0005198; F:structural molecule activity; IEA.  
DR GO:0016740; F:transferase activity; IEA.  
DR GO:0006350; P:transcription; IEA.  
DR GO:0019079; P:viral genome replication; IEA.  
DR InterPro; IPR007094; RNA\_pol\_PSVir.  
KW Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;  
KW Transferase.  
FT NON\_TER  
SQ SEQUENCE 3011 AA; 40406 MW; AD01ACDF4F73D95E CRC64;  
  
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Best Local Similarity 28.0%; Pred. No. 2.4;  
Matches 30; Conservative 12; Mismatches 32; Indels 33; Gaps 5;  
  
QY 2 HKPQSLDTPATLYAVVENVPLRWKFEVRL-----CLSDHEIDRLQLNGRCL 52  
DB 213 HK--ALDFD---MYGVNTITPLDLPQIIQRLHGMASFSLHSGYSGELNRV----GACL 262  
QY 53 REAQYSLMATWRRTTREPATELLGRVLRDMDLLGCLLEIDIEALCG 99  
DB 263 RKLGVPLPRAWHRARAVRAKLIQSG-----KAAICG 295  
  
RESULT 12  
Q81652 PRELIMINARY; PRT; 365 AA.  
ID Q81652  
AC Q81652  
DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
DE NS5 (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HC-G9;  
RA Okamoto H., Kojima M., Sakamoto M., Iizuka H., Hadiwandowo S.,  
Suwignyo S., Miyakawa Y., Mayumi M.;  
RT "The entire nucleotide sequence and classification of a hepatitis C  
RT virus isolate of a novel genotype from an Indonesian patient with  
RT chronic liver disease."  
RL J. Gen. Virol. 75:629-635 (1994).  
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
CC PROTEIN C AND RNA (BY SIMILARITY).  
DR EMBL; D14853; BAA03581.1; -  
DR PIR; P00804; P00804.  
DR HSP; P26663; IJXP.  
DR MEROPS; S29.001; -  
DR GO:0005524; F:ATP binding; IEA.  
DR GO:0008026; F:ATP dependent helicase activity; IEA.  
DR GO:0003723; F:RNA binding; IEA.  
DR GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
DR GO:0008236; F:serine-type peptidase activity; IEA.  
DR GO:0005198; F:structural molecule activity; IEA.  
DR GO:0016740; F:transferase activity; IEA.  
DR GO:0006350; P:transcription; IEA.  
DR GO:0019079; P:viral genome replication; IEA.  
DR InterPro; IPR007094; RNA\_pol\_PSVir.  
KW Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;  
KW Transferase.  
FT NON\_TER  
SQ SEQUENCE 365 AA; 40368 MW; EE7DF9DBC4186B9 CRC64;  
  
Query Match 14.0%; Score 81.5; DB 12; Length 365;  
Best Local Similarity 27.0%; Pred. No. 2.4;  
Matches 34; Conservative 13; Mismatches 38; Indels 41; Gaps 6;  
  
QY 2 HKPQSLDTPATLYAVVENVPLRWKFEVRL-GL-----SDHEIDRLQLNGRCL 52  
DB 212 HLEALDCE---IYCAVHSIQFLDLPETIIQRLHGLSAPLSHSYSGELNRV----AAAL 263  
QY 53 REAQYSLMATWRRTTREPATELLGRVLRDMDLLGCLLEIDIEALCG-----PAA 102

DR Pfam; PF01539; HCV env; 1.  
 DR Pfam; PF01560; HCV NS1; 1.  
 DR Pfam; PF01538; HCV NS2; 1.  
 DR Pfam; PF02907; HCV NS3; 1.  
 DR Pfam; PF01006; HCV NS4a; 1.  
 DR Pfam; PF01001; HCV NS4b; 1.  
 DR Pfam; PF01506; HCV NS5a; 1.  
 DR Pfam; PF00998; Viral\_RDRP; 1.  
 DR ProDom; PD186062; HCV NS1; 1.  
 DR SMART; SM00487; DEXDc; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
 KW Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.  
 FT CHAIN 1 191  
 FT CHAIN 192 383  
 FT CHAIN 384 809  
 FT CHAIN 810 1006  
 FT CHAIN 1007 1657  
 FT CHAIN 1658 1972  
 FT CHAIN 1973 3011  
 SQ SEQUENCE 3011 AA; 327212 MW; 9C16C120F4E79268 CRC64;

Query Match 14.0%; Score 81.5; DB 12; Length 3011;  
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 Matches 35; Conservative 11; Mismatches 39; Indels 41; Gaps 6;

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 Db HLEKALDCE---IYGAVHSVQPLDPEIIQLRLHGLSAFSLHSGYSGEINRV-----AACL 2909  
 QY 53 REAQYSLMATWRRTTPRRATLELLGRVLRMDLLGLCLEIDIEALCG-----PAA 102  
 Db RKLGVPLRAWRHRARVRATLLSQG-----RAACGKYLFWNAVKTKLK 2955

QY 103 LPPAPS 108  
 Db LTPLPS 2961

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 Q68798  
 ID Q68798 PRELIMINARY; PRT; 3022 AA.  
 AC Q68798;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Genome polyprotein.  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OX NCBI\_TaxID=11103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JK046;  
 RX MEDLINE=96226020; PubMed=8627233;  
 RA Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F.,  
 RA Lesmana L.A., Miyakawa Y., Mayumi M.;  
 RT "Hepatitis C virus variants from Jakarta, Indonesia classifiable into  
 RT novel genotypes in the second (2e and 2f), tenth (10a) and eleventh  
 RT (11a) genetic groups."  
 RL J. Gen. Virol. 77:293-301(1996).  
 CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
 CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
 CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
 CC PROTEIN C AND MRNA (BY SIMILARITY).  
 DR EMBL; D63822; BAA09891.1; -  
 DR HSSP; P27958; 1HEI.  
 DR MEROPS; S29.001; -  
 DR MEROPS; U39.001; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.

DR GO; GO:0003723; F:RNA binding; IEA.  
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
 DR GO; GO:0008236; F:serine-type peptidase activity; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.  
 DR GO; GO:0006350; P:transcription; IEA.  
 DR GO; GO:0019079; P:viral genome replication; IEA.  
 DR GO; GO:0019087; P:viral transformation; IEA.  
 DR InterPro; IPR009003; Cys Ser\_trypsin.  
 DR InterPro; IPR001410; DEAD.  
 DR InterPro; IPR002522; HCV capsid.  
 DR InterPro; IPR002521; HCV core.  
 DR InterPro; IPR002519; HCV env.  
 DR InterPro; IPR002531; HCV NS1.  
 DR InterPro; IPR002518; HCV NS2.  
 DR InterPro; IPR000745; HCV NS4a.  
 DR InterPro; IPR001490; HCV NS4b.  
 DR InterPro; IPR002868; HCV NS5a.  
 DR InterPro; IPR002166; HCV NS5.  
 DR InterPro; IPR004109; Peptidase C29.  
 DR InterPro; IPR007095; RNA\_pol\_DS\_PS.  
 DR InterPro; IPR007094; RNA\_pol\_PSVir.  
 DR Pfam; PF01543; HCV capsid; 1.  
 DR Pfam; PF01542; HCV core; 1.  
 DR Pfam; PF01539; HCV env; 1.  
 DR Pfam; PF01560; HCV NS1; 1.  
 DR Pfam; PF01538; HCV NS2; 1.  
 DR Pfam; PF02907; HCV NS3; 1.  
 DR Pfam; PF01006; HCV NS4a; 1.  
 DR Pfam; PF01001; HCV NS4b; 1.  
 DR Pfam; PF01506; HCV NS5a; 1.  
 DR Pfam; PF00998; Viral\_RDRP; 1.  
 DR ProDom; PD186062; HCV NS1; 1.  
 DR SMART; SM00487; DEXDc; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
 KW Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.  
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Query Match 14.0%; Score 81.5; DB 12; Length 3022;  
 Best Local Similarity 28.0%; Pred. No. 25;  
 Matches 30; Conservative 12; Mismatches 32; Indels 33; Gaps 5;

QY 2 HKPQSLDTPATLYAVVNPPLRWKEFVRRL-----GLSDHEIDRLQLNGRCL 52  
 Db HK-ALDCE---MYGVYNTITPLDLPQLRLHGLMAAFSLHSGYSGEINRV-----GACL 2920  
 QY 53 REAQYSLMATWRRTTPRRATLELLGRVLRMDLLGLCLEIDIEALCG 99  
 Db RKLGVPLRAWRHRARVRATLLSQG-----KAAICG 2953

RESULT 15  
 Q9KYP5  
 ID Q9KYP5 PRELIMINARY; PRT; 626 AA.  
 AC Q9KYP5;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Putative serine/threonine protein kinase.  
 GN SC04488 OR SC069.08.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Oliver K., Harris D.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);

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RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RL the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL coelicolor A3(2).";
RN Nature 417:141-147(2002).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AL939120; CAB92109.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008997; RicinB like.
DR InterPro; IPR000772; RicinB lectin.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00669; pkinase; 1.
DR Pfam; PF00652; RicinB_lectin; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS0231; RICIN_B_LECTIN; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase;
KW Complete proteome.
SQ SEQUENCE 626 AA; 63133 MW; 6FD66E3D3A1E44FE CRC64;

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Query Match 13.9%; Score 81; DB 16; Length 626;  
Best Local Similarity 29.1%; Pred. No. 4.9;  
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Db 74 --HELDNL-----ARLPEATAPLLAGDREARPPWATAVVGLTLREAVDLHGPLPAEAL 127
QY 93 ---TEELCGPAAL 103
Db 128 WLVLREAATGLAAV 141

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Search completed: June 1, 2004, 14:46:21  
Job time : 34.2335 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:30:06 ; Search time 48.521 Seconds  
(without alignments)  
646.376 Million cell updates/sec

Title: US-09-854-906-9

Perfect score: 557

Sequence: 1 ETWAINLSVDLSKYITIA.....KIQTILKDTSDSENSNFR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	557	100.0	111	5 ABB81750	Abb81750 Tumour ne
2	557	100.0	121	5 ABB81752	Abb81752 Tumour ne
3	557	100.0	314	2 AAR76238	Aar76238 Fas-delta
4	557	100.0	314	2 AAR99682	Aar99682 Human Fas
5	557	100.0	314	2 AAW98070	Aaw98070 Soluble F
6	557	100.0	335	2 AAR28084	Aar28084 Human cel
7	557	100.0	335	2 AAR78606	Aar78606 Human Fas
8	557	100.0	335	2 AAR99681	Aar99681 Human Fas
9	557	100.0	335	2 AAR95258	Aar95258 hFas from
10	557	100.0	335	2 AAW50289	Aaw50289 Human Fas
11	557	100.0	335	2 AAW49104	Aaw49104 Fas prote
12	557	100.0	335	3 AAB01335	Aab01335 CD-95 (FA
13	557	100.0	335	3 AAB19341	Aab19341 Amino aci
14	557	100.0	335	3 AAB36267	Aab36267 Human Fas
15	557	100.0	335	3 AAB50517	Aab50517 Human tum
16	557	100.0	335	6 ABU07407	Abu07407 Protein d
17	557	100.0	335	6 ABR43905	Abr43905 Human GEN
18	557	100.0	436	3 AAY91026	Aay91026 Apocobod
19	557	100.0	669	2 AAW64484	Aaw64484 Human TNF
20	550	98.7	431	4 AAY97650	Aay97650 CD44Hextr
21	550	98.7	431	6 ABU04641	Abu04641 Human exp
22	550	98.7	436	4 AAY97651	Aay97651 CD44Hextr
23	550	98.7	436	6 ABU04642	Abu04642 Human exp
24	550	98.7	920	4 AAY97652	Aay97652 Flt-lextr
25	550	98.7	927	4 AAY97653	Aay97653 Flk-lextr

26 541.5 97.2 331 4 AAB50893 Human Fas  
27 513 92.1 104 7 ADC08900 FAS prote  
28 427 76.7 84 4 AAY97654 Fas/Apo-1  
29 425 76.3 84 2 AAW62178 Fas-R pro  
30 393 70.6 77 6 ADA49710 Death dom  
31 386 69.3 77 5 ABG31494 Human Apo  
32 352 63.2 68 3 AAW93611 Human Fas  
33 352 63.2 68 3 AAB26988 Human CD9  
34 328 58.9 63 2 AAW00206 Human Fas  
35 278.5 50.0 327 2 AAR41688 Murine Fas  
36 278.5 50.0 327 2 AAR78611 Murine Fas  
37 278.5 50.0 327 2 AAR92530 mFas sequ  
38 278.5 50.0 327 2 AAW86241 Fas ligan  
39 278.5 50.0 327 3 AAB19344 Amino aci  
40 237 42.5 281 3 AAB26982 Human Fas  
41 180.5 32.4 37 4 AAY72885 Death dom  
42 86.5 15.5 1979 3 AAB18171 Plasmodiu  
43 80.5 14.5 67 3 AAY67948 Tumour ne  
44 80.5 14.5 656 2 AAW04627 Mouse rec  
45 80.5 14.5 656 2 AAW80994 Human rec

## ALIGNMENTS

### RESULT 1

ABB81750

ID ABB81750 standard; protein; 111 AA.

AC ABB81750;

XX ABB81750;

DT 10-SEP-2002 (first entry)

DB Tumour necrosis factor receptor Fas death domain (shorter sequence).

XX Tumour necrosis factor; receptor; TNFR-1; death domain; TNFR-1 DD; Fas;

XX Tumour necrosis factor; receptor; TNFR-1; death domain; TNFR-1 DD; Fas;

XX protein co-ordinate data.

XX Unidentified.

XX Unidentified.

PH Key

Region Location/Qualifiers

FT Region 14..22 /label= Alpha\_helix\_1

FT Region 25..34 /label= Alpha\_helix\_2

FT Region 39..47 /label= Alpha\_helix\_3

FT Region 57..68 /label= Alpha\_helix\_4

FT Region 73..83 /label= Alpha\_helix\_5

FT Region 89..101 /label= Alpha\_helix\_6

XX US2002045578-A1.

XX 18-APR-2002.

XX 14-MAY-2001; 2001US-00854906.

XX 22-MAY-2000; 2000US-0206215P.

XX (SUKI/) SUKITS S F.

XX (XUSG/) XILG.

XX (LINL/) LIN L.

XX (TELL/) TELLIEZ J.

XX (HSUS/) HSU S.

XX Sukits SF, Xu G, Lin L, Telliez J, Hsu S;

XX WPI; 2002-443412/47.

XX Solution comprising tumor necrosis factor receptor 1 death domain, useful





Db 197 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 256  
 QY 61 LRNWHQHGKKEAYDTLIKDLKKANLCTLAELKIQTIIILKDIITSDSENSNFR 111  
 Db 257 LRNWHQHGKKEAYDTLIKDLKKANLCTLAELKIQTIIILKDIITSDSENSNFR 307

RESULT 4  
 AAR99682  
 ID AAR99682 standard; protein; 314 AA.  
 AC AAR99682;  
 XX  
 DT 10-OCT-1996 (first entry)  
 XX  
 DE Human Fas soluble antigen Fas dell.  
 XX  
 KW Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;  
 KW angioimmunoblastic lymphadenopathy; ALLD.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..16  
 FT Protein /label= Sig\_peptide  
 FT 17..314  
 FT /label= Mat\_protein  
 FT /note= "soluble Fas dell antigen"  
 FT 17..168  
 FT /label= Extracellular domain  
 FT /note= "the 5 C-terminal residues of the Fas antigen  
 FT extracellular domain are deleted in Fas dell"  
 FT 161..171  
 FT Peptide /note= "preferred peptide from breakpoint region"  
 FT 164..174  
 FT Peptide /note= "preferred peptide from breakpoint region"  
 FT 164..173  
 FT /note= "preferred peptide from breakpoint region (claim  
 FT 4, page 132)"  
 FT 169..314  
 FT Domain /label= Cytoplasmic\_domain  
 XX  
 PN WO9620206-A1.  
 XX  
 PD 04-JUL-1996.  
 XX  
 PF 22-DEC-1995; 95WO-US017083.  
 XX  
 PR 23-DEC-1994; 94US-00371263.  
 XX  
 PA (UABR-) UAB RES FOUND.  
 XX  
 PI Mountz JD, Liu C, Zhou T, Cheng J;  
 XX  
 DR WPI; 1996-321796/32.  
 DR N-PSDB; AAT34527.  
 XX  
 PT Natural, soluble form of Fas antigen secreted by human cells is result of  
 PT alternative mRNA processing - used to diagnose Fas-associated disease,  
 PT e.g. systemic lupus erythematosus.  
 XX  
 PS Claim 4; Page 114-16; 152pp; English.  
 XX  
 CC A natural, soluble Fas antigen variant (AAR99682), designated Fas dell,  
 CC and other Fas variants (AAR99683-85) are derived by alternative splicing  
 CC of Fas gene transcripts. A cDNA clone (AAT34527) coding for the variant  
 CC was obcd. from human peripheral blood mononuclear cells. The Fas dell  
 CC variant lacks the transmembrane domain of insoluble Fas antigen  
 CC (AAR99681). Recombinant dell variant, or fragments of it, can be  
 CC expressed in prokaryotic or eukaryotic (e.g. COS) cells. Detection of  
 CC increased levels of soluble forms of Fas antigen can be used to diagnose  
 CC autoimmune diseases, esp. systemic lupus erythematosus and  
 CC angioimmunoblastic lymphadenopathy

XX SQ Sequence 314 AA;  
 Query Match 100.0%; Score 557; DB 2; Length 314;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-56;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
 Db 197 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 256  
 QY 61 LRNWHQHGKKEAYDTLIKDLKKANLCTLAELKIQTIIILKDIITSDSENSNFR 111  
 Db 257 LRNWHQHGKKEAYDTLIKDLKKANLCTLAELKIQTIIILKDIITSDSENSNFR 307

RESULT 5  
 AAW98070  
 ID AAW98070 standard; protein; 314 AA.  
 XX  
 AC AAW98070;  
 XX  
 DT 21-JUN-1999 (first entry)  
 XX  
 DE Soluble Fas receptor.  
 XX  
 KW Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive;  
 KW graft versus host disease; autoimmune disease; psoriasis;  
 KW rheumatoid arthritis; systemic lupus erythematosus; gene therapy.  
 XX  
 OS Mammalia.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..16  
 FT Protein /note= "signal peptide"  
 FT 17..314  
 FT /note= "mature protein"  
 FT Misc-difference 109  
 FT /note= "encoded by GAA"  
 FT Modified-site 118  
 FT /note= "N-glycosylated"  
 XX  
 PN WO9903999-A1.  
 XX  
 PD 28-JAN-1999.  
 XX  
 PF 16-JUL-1998; 98WO-US014771.  
 XX  
 PR 17-JUL-1997; 97US-0052829P.  
 XX  
 PA (UNMI ) UNIV MICHIGAN.  
 XX  
 PI Nabel GJ, Chen J;  
 XX  
 DR WPI; 1999-132243/11.  
 DR N-PSDB; AAX24878.  
 XX  
 PT Inhibition of proinflammatory responses - using an agent which modulates  
 PT FasL stimulation, used for treating graft versus host disease or  
 PT autoimmune disease.  
 XX  
 PS Disclosure; Fig 4B; 71pp; English.  
 XX  
 CC This present sequence is a soluble Fas receptor. The invention provides a  
 CC method for inhibiting a proinflammatory response in a cell mixture by  
 CC administering an immunosuppressive agent which inhibits the  
 CC proinflammatory activity of Fas ligand (FasL). In some embodiments, an  
 CC FasL is coadministered with the immunosuppressive agent, and the cell  
 CC mixture comprises neutrophil cells. The method can be practised in vitro,  
 CC ex vivo or in vivo. Suitable immunosuppressive agents include antisense  
 CC molecules that inhibit endogenous FasL expression, soluble Fas receptors  
 CC or variants, ribozymes that inhibit the endogenous expression of FasL,  
 CC drugs that inhibit FasL signalling, agents that induce the endogenous

CC expression of transforming growth factor (TGF)-beta, and polynucleotides  
 CC coding for an immunosuppressive agent such as TGF-beta. The method can be  
 CC used for treating diseases associated with an undesired FasL-mediated  
 CC proinflammatory response, e.g. graft versus host disease, or an  
 CC autoimmune disease such as systemic lupus erythematosus, rheumatoid  
 CC arthritis and psoriasis. The invention also provides a method for  
 CC identifying agents which modulate FasL stimulation of a proinflammatory  
 CC response  
 XX  
 SQ Sequence 314 AA;  
 Query Match 100.0%; Score 557; DB 2; Length 314;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-56;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKGVNEAKIDEIKNDNVQDTAEQKVL 60  
 Db 197 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKGVNEAKIDEIKNDNVQDTAEQKVL 256  
 QY 61 LRNWHQHGKKEAYDTLLKDKKANLCTLAETIQTILKDTSDSENSNFR 111  
 Db 257 LRNWHQHGKKEAYDTLLKDKKANLCTLAETIQTILKDTSDSENSNFR 307  
 RESULT 6  
 AAR28084  
 ID AAR28084 standard; protein; 335 AA.  
 XX  
 AC AAR28084;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 12-MAR-1993 (first entry)  
 DE Human cell surface antigen.  
 XX  
 KW Fas antigen; apoptosis; pF58; NGFR/TNFR family.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..16  
 FT Protein /label= signal  
 FT Domain /label= Fas\_antigen  
 FT /label= extracellular  
 FT /note= "cysteine-rich"  
 FT Modified-site 118..120  
 FT /label= N-glycosylation\_site  
 FT /note= "putative"  
 FT Modified-site 136..138  
 FT /label= N-glycosylation\_site  
 FT /note= "putative"  
 FT Domain 174..190  
 FT /label= transmembrane  
 FT Domain 191..335  
 FT /label= cytoplasmic  
 XX  
 PN EP510691-A1.  
 XX  
 PD 28-OCT-1992.  
 XX  
 PF 24-APR-1992; 92EP-00107060.  
 XX  
 PR 26-APR-1991; 91JP-00125234.  
 XX  
 PA (OSAB-) OSAKA BIOSCIENCE INST.  
 XX  
 PI Nagata S, Itoh N, Yonehara S;  
 XX  
 DR WPI; 1992-358914/44.  
 DR N-PSDB; AAQ29959.  
 XX

PT DNA encoding human cell surface antigen - used to clarify apoptosis  
 PT mechanism of various types of cell, and to prepare monoclonal antibodies  
 PT that react with tumour cells expressing Fas.  
 XX  
 PS Claim 3; Fig 1 and 2; 27pp; English.  
 XX  
 CC The Fas antigen is implicated in apoptosis. A cDNA clone encoding the  
 CC antigen was isolated (pF58) and the amino acid sequence of Fas was  
 CC deduced from it. The mature protein has a calculated mol.wt. of 36,000  
 CC and is a member of the NGFR/TNFR family of cell-surface membrane  
 CC proteins. The inventors claim a protein comprising at least the  
 CC extracellular domain of Fas antigen. (Updated on 25-MAR-2003 to correct  
 CC PN field.)  
 XX  
 SQ Sequence 335 AA;  
 Query Match 100.0%; Score 557; DB 2; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-56;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKGVNEAKIDEIKNDNVQDTAEQKVL 60  
 Db 218 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKGVNEAKIDEIKNDNVQDTAEQKVL 277  
 QY 61 LRNWHQHGKKEAYDTLLKDKKANLCTLAETIQTILKDTSDSENSNFR 111  
 Db 278 LRNWHQHGKKEAYDTLLKDKKANLCTLAETIQTILKDTSDSENSNFR 328  
 RESULT 7  
 AAR78606  
 ID AAR78606 standard; protein; 335 AA.  
 XX  
 AC AAR78606;  
 XX  
 DT 19-FEB-1996 (first entry)  
 DE Human Fas protein.  
 XX  
 KW Plasmid pF58; human Fas cDNA; soluble membrane protein;  
 KW antibody production; diseases; treatment; prevention.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..16  
 FT /label= sig\_peptide  
 FT Peptide 17..335  
 FT /label= mat\_peptide  
 XX  
 PN JP07115988-A.  
 XX  
 PD 09-MAY-1995.  
 XX  
 PF 26-OCT-1993; 93JP-00267644.  
 XX  
 PR 26-OCT-1993; 93JP-00267644.  
 XX  
 PA (NIBS ) JAPAN TOBACCO INC.  
 XX  
 DR WPI; 1995-202847/27.  
 DR N-PSDB; AAQ95297.  
 XX  
 PT Preparation of soluble membrane proteins - for their use in antibody  
 PT production for the treatment and prevention of related diseases.  
 XX  
 PS Example 1; Page 15-17; 51pp; Japanese.  
 XX  
 CC AAR78606 (human Fas protein) is encoded by the plasmid pF58 which  
 CC contains hFas cDNA. The plasmid was used in the construction of an  
 CC expression vector for the prodn. of recombinant soluble membrane  
 CC proteins. The proteins can be used in antibody prodn. for the treatment  
 CC and prevention of related diseases  
 CC

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XX SQ Sequence 335 AA;
Query Match 100.0%; Score 557; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. NO. 9.3e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
DB 218 ETVAINLSDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277

QY 61 LRNWHQLHGKKEAYDTLIKDKKANLCTLAETIOTIILKOITSDSENSNFR 111
DB 278 LRNWHQLHGKKEAYDTLIKDKKANLCTLAETIOTIILKOITSDSENSNFR 328

RESULT 8
AAR99681
ID AAR99681 standard; protein; 335 AA.
XX AC AAR99681;
XX DT 10-OCT-1996 (first entry)
XX DE Human Fas antigen.
XX KW Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;
XX KW angioimmunoblastic lymphadenopathy; AILD.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..16
XX FT /label= Sig_peptide
XX FT Protein 17..335
XX FT /label= Mat_protein
XX FT Domain 17..173
XX FT /label= Extracellular_domain
XX FT Domain 174..190
XX FT /label= Transmembrane_domain
XX FT Domain 191..335
XX FT /label= Cytoplasmic_tail
XX WO9620206-A1.
XX 04-JUL-1996.
XX 22-DEC-1995; 95WO-US017083.
XX 23-DEC-1994; 94US-00371263.
XX (UABR-) UAB RES FOUND.
XX Mountz JD, Liu C, Zhou T, Cheng J;
XX WPI; 1996-321796/32.
XX N-PSDB; AAT34526.
XX Natural, soluble form of Fas antigen secreted by human cells is result of
XX alternative mRNA processing - used to diagnose Fas-associated disease,
XX e.g. systemic lupus erythematosus.
XX Disclosure; Page 109-111; 152pp; English.
XX A CDNA clone (AAT34526) codes for a membrane receptor-like protein, Fas
XX antigen (AAR99681). It was isolated from cDNA derived from the peripheral
XX blood mononuclear cells of systemic lupus erythematosus (SLE) and
XX angioimmunoblastic lymphadenopathy (AILD) patients. 4 Soluble variants
XX (AAR99682-85) were identified of the Fas antigen. These arose by
XX alternative splicing of Fas gene transcripts. The Fas variants were
XX present at higher levels in SLE and AILD patients than the non-soluble
XX Fas antigen

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SQ Sequence 335 AA;
Query Match 100.0%; Score 557; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. NO. 9.3e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
DB 218 ETVAINLSDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277

QY 61 LRNWHQLHGKKEAYDTLIKDKKANLCTLAETIOTIILKOITSDSENSNFR 111
DB 278 LRNWHQLHGKKEAYDTLIKDKKANLCTLAETIOTIILKOITSDSENSNFR 328

RESULT 9
AAR92528
ID AAR92528 standard; protein; 335 AA.
XX AC AAR92528;
XX DT 06-SEP-1996 (first entry)
XX DE hFas from plasmid pCEV4/hFas.
XX KW Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
XX KW rheumatoid arthritis; serum; systemic lupus erythematosus.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Peptide 1..16
XX FT /notes= "hFas signal peptide"
XX FT Protein 17..335
XX FT /note= "mature hFas"
XX WO9601277-A1.
XX 18-JAN-1996.
XX 03-MAR-1995; 95WO-JP000349.
XX 06-JUL-1994; 94JP-00154706.
XX 14-FEB-1995; 95JP-00025637.
XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX (NISR) JAPAN TOBACCO INC.
XX Yonehara S, Noguchi J, Hachiya T;
XX WPI; 1996-087635/09.
XX N-PSDB; AAT16303.
XX Immunoassay method for soluble Fas antigen in body fluids - for diagnosis
XX of autoimmune diseases such as rheumatoid arthritis and systemic lupus
XX erythematosus.
XX Example 8; Page 49-52; 124pp; Japanese.
XX This sequence represents the sequence for the human Fas antigen contained
XX within the plasmid pCEV4/hFas. The soluble Fas antigen is included in the
XX immunoassay kit of the invention. The kit is for the assay of soluble Fas
XX antigen and contains an immobilised anti-soluble Fas monoclonal antibody,
XX as well as the standard soluble Fas antigen represented by this sequence.
XX The assay is simple and has high accuracy, high sensitivity, and is
XX capable of assaying a number of different specimens at the same time. The
XX immunoassay is used on biological samples (such as serum) and is useful
XX for diagnosis of autoimmune diseases such as rheumatoid arthritis or
XX systemic lupus erythematosus (SLE)
XX SQ Sequence 335 AA;
Query Match 100.0%; Score 557; DB 2; Length 335;

```

Best Local Similarity 100.0%; Pred. No. 9.3e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
DB 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
QY 61 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIILKDITSDSENSNFR 111  
DB 278 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIILKDITSDSENSNFR 328

RESULT 10  
AAW50289  
ID AAW50289 standard; protein; 335 AA.  
XX  
AC AAW50289;  
XX  
DT 16-JUL-1998 (first entry)  
XX  
DE Human Fas antigen.  
XX

KW Human; Fas antigen; derivative; apoptosis regulation; gene therapy;  
KW treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;  
KW apoptosis modulation.  
XX  
XX Homo sapiens.  
XX

Key Location/Qualifiers  
FH Peptide 1..16  
FT Peptide /label= sig\_peptide  
FT Peptide 17..335  
FT Peptide /label= mat\_peptide  
FT Region 17..173  
FT /note= "claimed fragment"

XX W09742319-A1.  
XX  
XX 13-NOV-1997.  
XX  
XX 01-MAY-1997; 97WO-JP001502.  
XX  
XX 02-MAY-1996; 96JP-00135760.  
XX  
XX (MOCH ) MOCHIDA PHARM CO LTD.  
XX (OSAB-) OSAKA BIOSCIENCE INST.  
XX  
XX Nakamura N, Nagata S;  
XX  
XX WPI; 1997-558981/51.  
XX N-PSDB; AAV07002.  
XX  
XX Fas antigen derivative containing modified extracellular region - has low  
XX antigenicity, promotes apoptosis and is useful in treatment of viral and  
XX other diseases.  
XX  
XX Claim 2; Fig 1-2; 102pp; Japanese.

XX The present sequence was used in the development of novel Fas antigen  
XX derivatives, which contain a Fas antigen extracellular region lacking one  
XX or more amino acid residues in the region from the amino-terminal to (but  
XX excluding) the 1st cysteine residue [preferably at least 29 residues (are  
XX deleted). The derivatives are effective regulators of apoptosis and can  
XX be used (either by administration of the polypeptide, or by the use of  
XX the coding DNA in gene therapy) to treat a range of diseases, e.g.  
XX diabetes, arthritis, lupus and in particular viral diseases such as  
XX hepatitis, influenza and HIV, by modulating apoptosis of virus-infected  
XX cells

XX Sequence 335 AA;

Query Match 100.0%; Score 557; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.3e-56;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
DB 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
QY 61 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIILKDITSDSENSNFR 111  
DB 278 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIILKDITSDSENSNFR 328

RESULT 11  
AAW49104  
ID AAW49104 standard; protein; 335 AA.

XX  
AC AAW49104;  
XX  
DT 27-AUG-2003 (revised)  
DT 18-NOV-1998 (first entry)  
XX  
DE Fas protein.  
XX

KW Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL;  
KW CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;  
KW simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;  
KW prophylactic; AIDS.  
XX  
XX Mammalia.  
XX

Key Location/Qualifiers  
FH Peptide 1..16  
FT Peptide /note= "Signal peptide"  
FT Protein 17..335  
FT Protein /note= "Fas protein"  
FT Region 17..172  
FT /note= "The portion of a Fas protein which can be fused  
FT to a Fc polypeptide to form a Fas-Fc fusion protein"

XX W09835692-A1.  
XX  
XX 20-AUG-1998.  
XX  
XX 17-FEB-1998; 98WO-GB000485.  
XX  
XX 17-FEB-1997; 97GB-00003276.  
XX (ISIS-) ISIS INNOVATION LTD.  
XX  
XX Screaton GR, Xu X;  
XX WPI; 1998-456867/39.  
XX N-PSDB; AAV32993.

XX Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency  
XX diseases - by interfering with interaction of Fas with Fas-ligand  
XX expressed on activated CD4+ cells, e.g. cells infected with HIV.

XX Disclosure; Fig 7; 71pp; English.

XX The present sequence represents a Fas protein sequence used in the method  
XX of the invention. The method is concerned with reducing depletion of  
XX activated Fas-expressing CD8+ T-lymphocyte killer (TK) cells in an immune  
XX cell population which also comprises of Fas-ligand (FasL)-expressing  
XX activated CD4+ cells. It involves contacting this immune cell population  
XX with an effective amount of an agent (e.g. a soluble Fas-Fc fusion  
XX protein) which would interfere with the interaction between Fas and FasL.  
XX Therefore, the method is useful for identifying suitable agents which can  
XX reduce depletion of activated Fas-expressing CD8+ TK cells in immune cell  
XX populations. Also claimed is the use of the agent in the manufacture of  
XX therapeutic compositions. Apoptosis of lymphocytes can be triggered by  
XX the interaction of the cell surface receptor Fas and its ligand FasL. By  
XX interfering with this interaction, the method described and its  
XX preparations can prevent apoptosis of CD8+ TK lymphocytes caused by

CC expression of FasL on activated CD4+ cells. Such FasL-expressing  
 CC activated CD4+ cells are especially the result of CD4+ cell infection  
 CC with an immunodeficiency virus e.g. human immunodeficiency virus (HIV) or  
 CC simian immunodeficiency virus (SIV). The claimed prevention of apoptosis  
 CC may then allow maintenance/regeneration of cytotoxic T lymphocyte (CTL)  
 CC activity towards the CD4+ cells infected with the infectious agent,  
 CC enabling treatment (prophylactic and/or therapeutic) of immunodeficiency  
 CC diseases e.g. AIDS. (Updated on 27-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 335 AA;

Query Match 100.0%; Score 557; DB 2; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-56;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
 |||||  
 Db 218 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277  
 |||||

QY 61 LRNHQHGKKEAYDTLIKDKKANLCTLAEKIQTIIILKDIITSDSENSNFR 111  
 |||||  
 Db 278 LRNHQHGKKEAYDTLIKDKKANLCTLAEKIQTIIILKDIITSDSENSNFR 328  
 |||||

RESULT 12  
 AAB01335  
 ID AAB01335 standard; protein; 335 AA.  
 AC AAB01335;  
 XX  
 XX 25-SEP-2000 (first entry)  
 DT  
 DE CD-95 (FAS/APO-1) death receptor.  
 XX

UL144; death receptor; apoptosis; programmed cell death; FAS; TNF-R1;  
 KW TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus; human.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200034335-A2.  
 PN  
 XX 15-JUN-2000.  
 PD

XX 03-DEC-1999; 99WO-US026035.  
 PF  
 XX 04-DEC-1998; 98US-00205018.  
 PR  
 XX (SCHE ) SCHERING CORP.  
 PA  
 XX Leong C, Phillips JH;  
 PI  
 XX WPI; 2000-423383/36.  
 DR

XX Purified or recombinant polypeptide for modulating apoptosis comprises a  
 PT sequence which binds to an antibody specific for Uli44 or its fragments.  
 PT  
 XX Disclosure; Page 64-65; 76pp; English.  
 PS

XX A pure or recombinant polypeptide which binds to a polyclonal antibody  
 CC specific for the mature Uli44 is useful for screening molecules which  
 CC block induction of apoptosis or interfere with antiapoptotic activity.  
 CC The polypeptide is also useful for modulating apoptosis and useful in  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, such as cancer or degenerative conditions and for regulation  
 CC of viral infection and replication. At least five different death  
 CC receptors are known, which include the CD95 (Fas/APO-1), the TNF receptor  
 CC -1, TNF receptor apoptosis-mediated protein (TRAMP), death receptor-6 (DR  
 CC -6), and TNF-related apoptosis-inducing ligand (TRAIL) receptors 1, 2 and  
 CC 4

XX Sequence 335 AA;

Query Match 100.0%; Score 557; DB 3; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.3e-56;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
 |||||  
 Db 218 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277  
 |||||

QY 61 LRNHQHGKKEAYDTLIKDKKANLCTLAEKIQTIIILKDIITSDSENSNFR 111  
 |||||  
 Db 278 LRNHQHGKKEAYDTLIKDKKANLCTLAEKIQTIIILKDIITSDSENSNFR 328  
 |||||

RESULT 13  
 AAB19341  
 ID AAB19341 standard; protein; 335 AA.  
 AC AAB19341;  
 XX  
 XX 06-MAR-2001 (first entry)  
 DT

DE Amino acid encoding a human Fas (Apo-1) protein.  
 XX  
 XX Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis;  
 KW Fas associated protein 1; protein tyrosine phosphatase; cancer;  
 KW autoimmune disease; inflammatory disease; lymphoma.  
 XX

OS Homo sapiens.  
 XX  
 XX WO2000061150-A1.  
 PN  
 XX 19-OCT-2000.  
 PD

XX 10-APR-2000; 2000WO-US009540.  
 PF  
 XX 12-APR-1999; 99US-00290640.  
 PR

XX (ISIS-) ISIS PHARM INC.  
 PA  
 XX Dean NM, Marcussen EG;  
 PI  
 XX WPI; 2000-628395/60.  
 DR  
 XX N-PSDB; AAC61798.

XX Antisense oligonucleotides for treating hepatitis and colon, liver or  
 PT lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein 1  
 PT (Fap-1) expression.  
 XX

PS Example 2; Page 73-74; 116pp; English.

XX The present sequence represents human Fas (Apo-1). The specification  
 CC describes antisense compounds which are targeted to the 5'-untranslated  
 CC region, translational start site, translational termination region or 3'-  
 CC untranslated region of nucleic acid molecules encoding Fas, Fas ligand  
 CC (FasL), or Fap-1 (Fas associated protein 1, protein tyrosine  
 CC phosphatase). The antisense compounds are used to inhibit the expression  
 CC of Fas, FasL or Fap-1 in cells or tissues. They are used to treat  
 CC autoimmune or inflammatory diseases such as hepatitis. They can also be  
 CC used to treat cancer, especially colon, liver or lung cancer or lymphoma  
 XX

SQ Sequence 335 AA;

Query Match 100.0%; Score 557; DB 3; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-56;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
 |||||  
 Db 218 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277  
 |||||

QY 61 LRNHQHGKKEAYDTLIKDKKANLCTLAEKIQTIIILKDIITSDSENSNFR 111  
 |||||  
 Db 278 LRNHQHGKKEAYDTLIKDKKANLCTLAEKIQTIIILKDIITSDSENSNFR 328  
 |||||

## RESULT 14

AAB36267  
ID AAB36267 standard; protein; 335 AA.

AC AAB36267;  
AC

DT 20-FEB-2001 (first entry)

DE Human Fas receptor.

XX Human; death domain containing receptor; DR3-V1; cancer;  
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;  
KW neurodegenerative disease; angiogenesis.

OS Homo sapiens.

PN WO200064465-A1.

XX 02-NOV-2000.

PF 21-APR-2000; 2000WO-US010741.

XX 22-APR-1999; 99US-0130488P.

PR 28-MAY-1999; 99US-0136741P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.

PA (YUGG/) YU G.

PA (NIGU/) NI J.

PA (GENT/) GENTZ R L.

PA (DILL/) DILLON P J.

PA (DIXI/) DIXIT V M.

XX Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;  
PI

XX WPI; 2000-687263/67.

XX Treating graft-versus-host disease, cancer, immunodeficiency or an  
PT autoimmune disease comprising administering an antibody to Death Domain  
PT Containing Receptor proteins and a second therapeutic agent.

PS Disclosure; Fig 3; 273pp; English.

XX The present invention provides the protein and coding sequences for two  
CC death domain containing receptors, designated DR3 and DR3-V1. These  
CC receptors are involved in apoptosis, and the sequences given can be used  
CC in the treatment of cancers, infections, cardiovascular disorders such as  
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms  
CC and congenital heart defects, neurodegenerative diseases including  
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple  
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,  
CC and to promote angiogenesis and wound healing

XX Sequence 335 AA;

Query Match 100.0%; Score 557; DB 3; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.3e-56;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60

DB 218 ETVAINLSDVLSKYITTTAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277

QY 61 LRNWHQHGKKEAYDTLTKDLKKNLCTLAETIQTIIILKDTSDSENFR 111

DB 278 LRNWHQHGKKEAYDTLTKDLKKNLCTLAETIQTIIILKDTSDSENFR 328

## RESULT 15

AAB50517  
ID AAB50517 standard; protein; 335 AA.

XX

AC

AAB50517;

XX 15-MAR-2001 (first entry)

DE Human tumour necrosis factor receptor FAS protein SEQ ID NO:7.

XX Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nontropic;  
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;  
KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;  
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;  
KW anticonvulsant; antiparasitic; cardiac; anti-HIV; antiparkinsonian;  
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;  
KW apoptotic cell death related disease; autoimmune disorder;  
KW cardiovascular disorder; viral infection.

XX Homo sapiens.

XX WO200071150-A1.

XX 30-NOV-2000.

XX 18-MAY-2000; 2000WO-US013515.

XX 20-MAY-1999; 99US-0135164P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Wei Y, Ruben SM, Gentz RL, Ni J;  
PI

XX WPI; 2001-041051/05.

XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor  
PT necrosis factor receptor 5, useful in the diagnosis, treatment or  
PT prevention of cancer, autoimmune disorders and viral infection.

XX Disclosure; Fig 2; 285pp; English.

XX The present invention describes the human TRID protein (tumour necrosis  
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
CC intracellular domain, also referred to as tumour necrosis factor receptor  
CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nontropic,  
CC neuroprotective, antiviral, antiinflammatory, anticonvulsant,  
CC antiparasitic, cardiac, anti-HIV, antiparkinsonian and vasotropic  
CC activities, and can be used in gene therapy. The TRID polynucleotides are  
CC useful for detecting complementary polynucleotides. TRID proteins and  
CC polynucleotides are useful in the treatment of tumours, resistance to  
CC parasite, bacteria and viruses, restenosis and graft versus host disease.  
CC They are also useful for inducing proliferation of T-cells, endothelial  
CC cells and certain haematopoietic cells, to regulate antiviral responses  
CC and to prevent certain autoimmune diseases after stimulation of TRID by  
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID  
CC polypeptides are useful for treating and/or preventing diseases  
CC associated with increased or decreased apoptotic cell death. The TRID  
CC polynucleotides, proteins, antibodies, agonists and antagonists are  
CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)  
CC autoimmune disorders; (c) diseases associated with increased apoptosis;  
CC (d) cardiovascular disorders; and (e) viral infection. The present  
CC sequence represents a tumour necrosis factor receptor used in comparison  
CC with TRID in the exemplification of the present invention

XX Sequence 335 AA;

Query Match 100.0%; Score 557; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.3e-56;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60

DB 218 ETVAINLSDVLSKYITTTAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277

QY 61 LRNWHQHGKKEAYDTLTKDLKKNLCTLAETIQTIIILKDTSDSENFR 111

DB 278 LRNWHQHGKKEAYDTLTKDLKKNLCTLAETIQTIIILKDTSDSENFR 328

Search completed: June 1, 2004, 14:43:53  
Job time : 49.521 secs

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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:41:22 ; Search time 13.9581 Seconds  
(without alignments)  
410.549 Million cell updates/sec

Title: US-09-854-906-9

Perfect score: 557

Sequence: 1 ETVAINLSVDLSKYITIA.....KIQTILKDTSDSENSNFR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.\*
- 1: /cgn2\_6/ptodata/2/iaa/5A.COMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/iaa/5B.COMB.pep.\*
  - 3: /cgn2\_6/ptodata/2/iaa/6A.COMB.pep.\*
  - 4: /cgn2\_6/ptodata/2/iaa/6B.COMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/iaa/PCTUS.COMB.pep.\*
  - 6: /cgn2\_6/ptodata/2/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	100.0	314	1	US-08-444-231-19
2	557	100.0	314	1	US-08-152-443A-19
3	557	100.0	314	5	PCT-US95-17083-4
4	557	100.0	335	2	US-08-219-237B-2
5	557	100.0	335	2	US-08-409-338-1
6	557	100.0	335	3	US-08-815-469-6
7	557	100.0	335	3	US-08-230-640-2
8	557	100.0	335	3	US-08-006-353A-7
9	557	100.0	335	3	US-08-468-560C-2
10	557	100.0	335	4	US-09-180-100-20
11	557	100.0	335	4	US-09-565-918-3
12	557	100.0	335	4	US-09-573-986-7
13	557	100.0	335	4	US-09-665-615B-2
14	557	100.0	335	5	PCT-US95-17083-4
15	557	100.0	669	4	US-09-013-895A-3
16	557	100.0	669	4	US-09-448-868-3
17	541.5	97.2	331	3	US-09-086-483A-3
18	541.5	97.2	331	4	US-09-580-212-3
19	541.5	97.2	331	4	US-09-769-402-3
20	431	77.4	85	3	US-09-042-785A-26
21	425	76.3	84	4	US-09-828-683A-119
22	393	70.6	77	4	US-08-828-683A-24
23	361	64.8	70	4	US-09-159-277A-5
24	352	63.2	68	4	US-09-527-236A-22
25	352	63.2	68	4	US-09-756-854-22
26	328	58.9	63	4	US-08-894-626-1
27	278.5	50.0	327	3	US-09-290-640-66

28	278.5	50.0	327	4	US-09-665-615B-66	Sequence 66, Appl
29	237	42.5	45	2	US-08-219-237B-10	Sequence 10, Appl
30	237	42.5	281	4	US-09-527-236A-3	Sequence 3, Appl
31	237	42.5	281	4	US-09-756-854-3	Sequence 3, Appl
32	212	38.1	40	1	US-08-444-005-27	Sequence 27, Appl
33	182	32.7	70	4	US-09-159-277A-4	Sequence 4, Appl
34	167	30.0	41	1	US-08-444-005-33	Sequence 33, Appl
35	137	24.6	40	1	US-08-444-005-26	Sequence 26, Appl
36	122	21.9	25	1	US-08-444-005-21	Sequence 21, Appl
37	82	14.7	261	4	US-09-634-238-420	Sequence 420, Appl
38	80.5	14.5	656	1	US-08-444-005-15	Sequence 15, Appl
39	80.5	14.5	656	4	US-09-069-023-28	Sequence 28, Appl
40	80.5	14.5	656	4	US-09-345-473E-30	Sequence 30, Appl
41	78.5	14.1	77	3	US-08-995-159-7	Sequence 7, Appl
42	78.5	14.1	77	4	US-09-545-605-7	Sequence 7, Appl
43	78.5	14.1	87	3	US-09-042-785A-29	Sequence 29, Appl
44	78.5	14.1	671	3	US-09-132-118-2	Sequence 2, Appl
45	78.5	14.1	671	4	US-09-345-473E-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1  
US-08-444-231-19  
; Sequence 19, Application US/08444231  
; Patent No. 5652210  
; GENERAL INFORMATION:  
; APPLICANT: BARR, PHILIP J.  
; APPLICANT: SHAPIRO, JOHN P.  
; APPLICANT: KIEFER, MICHAEL C.  
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,231  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/152,443  
; FILING DATE: 15-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20006.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 314 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-444-231-19

Query Match 100.0%; Score 557; DB 1; Length 314;  
Best Local Similarity 100.0%; Pred. No. 4.5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTAGVMTLSQVKGFRKGVNEAKIDEIKNDNVQDTAEQKVL 60  
Db 197 ETVAINLSVDLSKYITTTAGVMTLSQVKGFRKGVNEAKIDEIKNDNVQDTAEQKVL 256

QY 61 LRNVHQLHGKKEAYDTLLKDKKANLCTLAEKIQTIIILKDIITSDSENSNFR 111  
Db 257 LRNVHQLHGKKEAYDTLLKDKKANLCTLAEKIQTIIILKDIITSDSENSNFR 307

RESULT 2  
US-08-152-443A-19  
; Sequence 19, Application US/08152443A  
; Patent No. 5663070  
; GENERAL INFORMATION:  
; APPLICANT: BARR, PHILIP J.  
; APPLICANT: SHAPIRO, JOHN P.  
; APPLICANT: KIEFER, MICHAEL C.  
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FORSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/152,443A  
; FILING DATE: 15-NOV-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20006.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 314 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-152-443A-19

Query Match 100.0%; Score 557; DB 1; Length 314;  
Best Local Similarity 100.0%; Pred. No. 4.5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTAGVMTLSQVKGFRKGVNEAKIDEIKNDNVQDTAEQKVL 60  
Db 197 ETVAINLSVDLSKYITTTAGVMTLSQVKGFRKGVNEAKIDEIKNDNVQDTAEQKVL 256

QY 61 LRNVHQLHGKKEAYDTLLKDKKANLCTLAEKIQTIIILKDIITSDSENSNFR 111  
Db 257 LRNVHQLHGKKEAYDTLLKDKKANLCTLAEKIQTIIILKDIITSDSENSNFR 307

RESULT 3  
PCT-US95-17083-4  
; Sequence 4, Application PC/TUS9517083  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/17083  
; FILING DATE: CONCURRENTLY HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/371,263  
; FILING DATE: 23-DEC-1994  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 314 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
PCT-US95-17083-4

Query Match 100.0%; Score 557; DB 5; Length 314;  
Best Local Similarity 100.0%; Pred. No. 4.5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTAGVMTLSQVKGFRKGVNEAKIDEIKNDNVQDTAEQKVL 60  
Db 197 ETVAINLSVDLSKYITTTAGVMTLSQVKGFRKGVNEAKIDEIKNDNVQDTAEQKVL 256

QY 61 LRNVHQLHGKKEAYDTLLKDKKANLCTLAEKIQTIIILKDIITSDSENSNFR 111  
Db 257 LRNVHQLHGKKEAYDTLLKDKKANLCTLAEKIQTIIILKDIITSDSENSNFR 307

RESULT 4  
US-08-219-237B-2  
; Sequence 2, Application US/08219237B  
; Patent No. 5874546  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu  
; APPLICANT: ITOH, Naoto  
; APPLICANT: YONEHARA, Shin  
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James W. Hellwege  
; STREET: P.O. Box 2266 Eads Station  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/219,237B  
; FILING DATE: 28-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/872,129  
; FILING DATE: 22-APR-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James W. Hellwege  
; REGISTRATION NUMBER: 28,808  
; REFERENCE/DOCKET NUMBER: 516762  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 335 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-219-237B-2

Query Match 100.0%; Score 557; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTAGVMTLSQVKGFRKGVNEAKIDEIKNDNVQDTAEQKVL 60

Db 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277  
QY 61 LRNWHQHGKKEAYDTLILKOLKCANLCTLAETIOTIILKIDITSSENSFR 111  
Db 278 LRNWHQHGKKEAYDTLILKOLKCANLCTLAETIOTIILKIDITSSENSFR 328

RESULT 5  
US-08-409-338-1  
; Sequence 1, Application US/08409338  
; Patent No. 5891434  
; GENERAL INFORMATION:  
; APPLICANT: Krammer, Peter H.  
; APPLICANT: Debatin, Klaus-Michael  
; APPLICANT: Trauth, Bernhard C.  
; APPLICANT: Behrmann, Iris  
; APPLICANT: Dhein, Jens  
; APPLICANT: Klas, Christiane  
; APPLICANT: Mller, Peter  
; APPLICANT: Falk, Werner  
; APPLICANT: Oehm Alexander  
; APPLICANT: Daniel, Peter T.  
; TITLE OF INVENTION: Monoclonal Antibodies to the APO-1 Antigen  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington, MA 02173  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/409,338  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,644  
; FILING DATE: 16-JUN-1994  
; APPLICATION NUMBER: US 07/691,016  
; FILING DATE: 17-JUN-1991  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: CTR89-35A2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 335 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-409-338-1  
Query Match 100.0%; Score 557; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
Db 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277

QY 61 LRNWHQHGKKEAYDTLILKOLKCANLCTLAETIOTIILKIDITSSENSFR 111  
Db 278 LRNWHQHGKKEAYDTLILKOLKCANLCTLAETIOTIILKIDITSSENSFR 328

RESULT 6  
US-08-815-469-6  
; Sequence 6, Application US/08815469  
; Patent No. 6153402  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,469  
; FILING DATE: HEREMITH  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 6153402 Yet Assigned  
; FILING DATE: 06-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/028,711  
; FILING DATE: 17-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/013,285  
; FILING DATE: 12-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 335 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
US-08-815-469-6  
Query Match 100.0%; Score 557; DB 3; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
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QY 61 LRNWHQHGKKEAYDTLILKOLKCANLCTLAETIOTIILKIDITSSENSFR 111  
Db 278 LRNWHQHGKKEAYDTLILKOLKCANLCTLAETIOTIILKIDITSSENSFR 328

RESULT 7  
US-09-290-640-2  
; Sequence 2, Application US/09290640  
; Patent No. 6204055  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.

APPLICANT: Marcusson, Eric G.  
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-0351  
CURRENT APPLICATION NUMBER: US/09/290,640  
CURRENT FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 335  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-290-640-2

Query Match 100.0%; Score 557; DB 3; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56; Indels 0; Gaps 0;  
Matches 111; Conservative 0; Mismatches 0;

QY 1 ETVAIINLSDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
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QY 61 LRNVHQLHGKKEAYDTLLKDLKANKLCTLAETKIQTIIILKDIITSDSENSNFR 111  
DB 278 LRNVHQLHGKKEAYDTLLKDLKANKLCTLAETKIQTIIILKDIITSDSENSNFR 328

RESULT 8  
US-09-006-353A-7  
Sequence 7, Application US/09006353A  
Patent No. 6261801  
GENERAL INFORMATION:  
APPLICANT: WEI, YING-FEI  
APPLICANT: YU, GUO-LIANG  
APPLICANT: GENTZ, REINER  
APPLICANT: RUBEN, STEVEN  
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,353A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF341  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 335 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-006-353A-7

Query Match 100.0%; Score 557; DB 3; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 218 ETVAIINLSDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277  
QY 61 LRNVHQLHGKKEAYDTLLKDLKANKLCTLAETKIQTIIILKDIITSDSENSNFR 111  
DB 278 LRNVHQLHGKKEAYDTLLKDLKANKLCTLAETKIQTIIILKDIITSDSENSNFR 328

RESULT 9  
US-08-468-560C-2  
Sequence 2, Application US/08468560C  
Patent No. 6270998  
GENERAL INFORMATION:  
APPLICANT: NAGATA, Shigekazu  
APPLICANT: ITOH, Naoto  
APPLICANT: YONEHARA, Shin  
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE  
TITLE OF INVENTION: ANTIGEN  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.  
STREET: P.O. BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,560C  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR., GERLAD M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 20-4393P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 335 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-560C-2

Query Match 100.0%; Score 557; DB 3; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56; Indels 0; Gaps 0;  
Matches 111; Conservative 0; Mismatches 0;

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DB 218 ETVAIINLSDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277  
QY 61 LRNVHQLHGKKEAYDTLLKDLKANKLCTLAETKIQTIIILKDIITSDSENSNFR 111  
DB 278 LRNVHQLHGKKEAYDTLLKDLKANKLCTLAETKIQTIIILKDIITSDSENSNFR 328

RESULT 10  
US-09-180-100-20  
Sequence 20, Application US/09180100  
Patent No. 6306395  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, No. 6306395  
APPLICANT: NAGATA, Shigekazu  
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE  
FILE REFERENCE: 1110-207P

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; CURRENT APPLICATION NUMBER: US/09/180,100
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-20

Query Match      100.0%; Score 557; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 5e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277

QY 61 LRNWHQHGKKEAYDTLLIKLKKANLCTLAEKIQTIIKDIITSDSENSNFR 111
Db 278 LRNWHQHGKKEAYDTLLIKLKKANLCTLAEKIQTIIKDIITSDSENSNFR 328

RESULT 11
US-09-565-918-3
; Sequence 3, Application US/09565918
; Patent No. 6433147
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/09/565,918
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-03-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-918-3

Query Match      100.0%; Score 557; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 5e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 278 LRNWHQHGKKEAYDTLLIKLKKANLCTLAEKIQTIIKDIITSDSENSNFR 328

RESULT 12
US-09-573-986-7
; Sequence 7, Application US/09579986
; Patent No. 6455040
; GENERAL INFORMATION:
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; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-7

Query Match      100.0%; Score 557; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 5e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 278 LRNWHQHGKKEAYDTLLIKLKKANLCTLAEKIQTIIKDIITSDSENSNFR 328

RESULT 13
US-09-665-615B-2
; Sequence 2, Application US/09665615B
; Patent No. 6653133
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0502
; CURRENT APPLICATION NUMBER: US/09/665,615B
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-665-615B-2

Query Match      100.0%; Score 557; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 5e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
PCT-US95-17083-2
; Sequence 2, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
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;; FILING DATE: CONCURRENTLY HERewith  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: USN 08/371,263  
;; FILING DATE: 23-DEC-1994  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 335 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
PCT-US95-17083-2

Query Match 100.0%; Score 557; DB 5; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 218 ETVAINLSVDLSKYITTTAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277  
QY 61 LRNWHQHGKKEAYDTLTKDLKKNLCTLAETIILKDIITSDSENSNFR 111  
Db 278 LRNWHQHGKKEAYDTLTKDLKKNLCTLAETIILKDIITSDSENSNFR 328

RESULT 15  
US-09-013-895A-3  
; Sequence 3, Application US/09013895A  
; Patent No. 6342363  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Pan, James G.  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dixit, Vishva M.  
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death  
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor  
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/013,895A  
; FILING DATE: 27-JAN-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC X.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1300002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 669 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-013-895A-3

Query Match 100.0%; Score 557; DB 4; Length 669;  
Best Local Similarity 100.0%; Pred. No. 1.2e-55;

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Job time : 14.9581 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 14:43:57 ; Search time 35,8922 Seconds

(without alignments)  
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Title: US-09-854-906-9

Perfect score: 557

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	557	100.0	335	9 US-09-802-669-2	Sequence 2, Appli
3	557	100.0	335	9 US-09-333-966-6	Sequence 6, Appli
4	557	100.0	335	9 US-09-949-713-20	Sequence 20, Appli
5	557	100.0	335	9 US-09-874-138-4	Sequence 4, Appli
6	557	100.0	335	9 US-09-884-987-2	Sequence 2, Appli
7	557	100.0	335	10 US-09-935-727-9	Sequence 9, Appli
8	557	100.0	335	10 US-09-314-889-6	Sequence 6, Appli
9	557	100.0	335	12 US-10-619-220-2	Sequence 2, Appli
10	557	100.0	335	13 US-10-005-842-4	Sequence 4, Appli
11	557	100.0	335	14 US-10-175-902-3	Sequence 7, Appli
12	557	100.0	335	14 US-10-186-643-7	Sequence 3, Appli
13	557	100.0	335	14 US-10-189-189-6	Sequence 6, Appli
14	557	100.0	335	15 US-10-418-242-9	Sequence 9, Appli
15	557	100.0	669	14 US-10-226-296-3	Sequence 3, Appli

16	557	100.0	669	14	US-10-226-318-3	Sequence 3, Appli
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18	515	92.5	104	15	US-10-359-439-2	Sequence 2, Appli
19	393	70.6	77	12	US-10-207-295-11	Sequence 11, Appli
20	393	70.6	77	13	US-10-112-793-24	Sequence 24, Appli
21	386	69.3	77	9	US-09-887-879-17	Sequence 17, Appli
22	386	69.3	77	9	US-09-992-964-17	Sequence 17, Appli
23	386	69.3	77	14	US-10-242-383-17	Sequence 17, Appli
24	352	63.2	68	9	US-09-756-854-22	Sequence 22, Appli
25	352	63.2	68	13	US-10-041-574-22	Sequence 22, Appli
26	328	58.9	63	13	US-10-035-408-1	Sequence 1, Appli
27	278.5	50.0	327	9	US-09-802-669-66	Sequence 66, Appli
28	278.5	50.0	327	12	US-10-619-220-66	Sequence 66, Appli
29	237	42.5	281	9	US-09-756-854-3	Sequence 3, Appli
30	237	42.5	281	13	US-10-041-574-3	Sequence 3, Appli
31	118	21.2	95	12	US-10-087-684-87	Sequence 87, Appli
32	118	21.2	95	12	US-10-218-779-87	Sequence 87, Appli
33	118	21.2	95	12	US-09-972-211-128	Sequence 128, Appli
34	118	21.2	95	12	US-10-096-625-128	Sequence 128, Appli
35	118	21.2	96	11	US-09-970-944-45	Sequence 45, Appli
36	118	21.2	96	12	US-10-037-417-124	Sequence 124, Appli
37	84.5	15.2	83	11	US-09-970-944-47	Sequence 47, Appli
38	84.5	15.2	83	12	US-10-037-417-126	Sequence 126, Appli
39	84.5	15.2	276	15	US-10-264-213-242	Sequence 242, Appli
40	83.5	15.0	82	12	US-10-087-684-89	Sequence 89, Appli
41	83.5	15.0	82	12	US-10-218-779-89	Sequence 89, Appli
42	82	14.7	261	15	US-10-264-213-227	Sequence 227, Appli
43	80.5	14.5	656	9	US-09-862-027-30	Sequence 30, Appli
44	80.5	14.5	1182	12	US-10-282-122A-53445	Sequence 53445, A
45	78.5	14.1	77	14	US-10-287-594-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-09-826-212-7  
; Sequence 7, Application US/09826212  
; Patent No. US20010021516A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: Gentz, Reiner  
; APPLICANT: Ruben, Steven  
; APPLICANT: Ni, Jian  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
; FILE REFERENCE: 1488.1280006  
; CURRENT APPLICATION NUMBER: US/09/826,212  
; CURRENT FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 7  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-826-212-7

Query Match 100.0%; Score 557; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 4,1e-51;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ETVAINLSVDLSKYITTTIAGVMTLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVQL 60  
Db 218 ETVAINLSVDLSKYITTTIAGVMTLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVQL 277  
Qy 61 LRNWHQLHGKKEAYDTLIDKLNKLCIAETIQLKIDTSSENSFR 111  
Db 278 LRNWHQLHGKKEAYDTLIDKLNKLCIAETIQLKIDTSSENSFR 328

RESULT 2  
US-09-802-669-2  
; Sequence 2, Application US/09802669  
; Patent No. US20020004490A1

GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcussen, Eric G.  
; APPLICANT: Wyatt, Jacqueline  
; APPLICANT: Zhang, Hong  
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-545  
; CURRENT APPLICATION NUMBER: US/09/802,669  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: US 09/665,615  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US 09/290,640  
; PRIOR FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-802-669-2

Query Match 100.0%; Score 557; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 4.1e-51;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQL 60  
Db 218 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQL 277

QY 61 LRNWHQHGKKEAYDTLIKDKKANLCTLAETKIQTIIILKDIITSDSENSNFR 111  
Db 278 LRNWHQHGKKEAYDTLIKDKKANLCTLAETKIQTIIILKDIITSDSENSNFR 328

RESULT 3  
US-09-333-966-6  
; Sequence 6, Application US/09333966  
; Patent No. US20020009773A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillion, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/333,966  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,469  
; FILING DATE:  
; APPLICATION NUMBER: No. US20020009773A1 Yet Assigned  
; FILING DATE: 06-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/028,711  
; FILING DATE: 17-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/013,285  
; FILING DATE: 12-MAR-1996

ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 335 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: No. US20020009773A1 Relevant  
; TOPOLOGY: No. US20020009773A1 Relevant  
; MOLECULE TYPE: protein  
US-09-333-966-6

Query Match 100.0%; Score 557; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 4.1e-51;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQL 60  
Db 218 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQL 277

QY 61 LRNWHQHGKKEAYDTLIKDKKANLCTLAETKIQTIIILKDIITSDSENSNFR 111  
Db 278 LRNWHQHGKKEAYDTLIKDKKANLCTLAETKIQTIIILKDIITSDSENSNFR 328

RESULT 4  
US-09-949-713-20  
; Sequence 20, Application US/09949713  
; Patent No. US20020044944A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, No. US20020044944A1  
; APPLICANT: NAGATA, Shigekazu  
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE  
; FILE REFERENCE: 1110-207P  
; CURRENT APPLICATION NUMBER: US/09/949,713  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US/09/180,100  
; PRIOR FILING DATE: 1998-11-02  
; PRIOR APPLICATION NUMBER: PCT/JP97/01502  
; PRIOR FILING DATE: 1997-05-01  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-949-713-20

Query Match 100.0%; Score 557; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 4.1e-51;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQL 60  
Db 218 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQL 277

QY 61 LRNWHQHGKKEAYDTLIKDKKANLCTLAETKIQTIIILKDIITSDSENSNFR 111  
Db 278 LRNWHQHGKKEAYDTLIKDKKANLCTLAETKIQTIIILKDIITSDSENSNFR 328

RESULT 5  
US-09-874-138-4  
; Sequence 4, Application US/09874138  
; Patent No. US20020072091A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Yu, Guo-Liang



; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Death Domain Containing Receptor 5  
; FILE REFERENCE: 1488.1310006  
; CURRENT APPLICATION NUMBER: US/09/874,138  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/565,009  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/148,939  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: 60/133,238  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/132,498  
; PRIOR FILING DATE: 1999-05-04  
; PRIOR APPLICATION NUMBER: 09/042,583  
; PRIOR FILING DATE: 1998-03-17  
; PRIOR APPLICATION NUMBER: 60/054,021  
; PRIOR FILING DATE: 1997-07-29  
; PRIOR APPLICATION NUMBER: 60/040,846  
; PRIOR FILING DATE: 1997-03-17  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-874-138-4

Query Match 100.0%; Score 557; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 4.1e-51;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db 218 ETVAINLSVDLSKYITTIAGVMTLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
  
QY 61 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIILKDTSDSENSFR 111  
Db 278 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIILKDTSDSENSFR 328

RESULT 6  
US-09-884-987-2  
; Sequence 2, Application US/09884987  
; Patent No. US20020102653A1  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu et al  
; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN  
; FILE REFERENCE: 0020-4877P  
; CURRENT APPLICATION NUMBER: US/09/884,987  
; CURRENT FILING DATE: 2001-06-21  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-884-987-2

Query Match 100.0%; Score 557; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 4.1e-51;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db 218 ETVAINLSVDLSKYITTIAGVMTLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
  
QY 61 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIILKDTSDSENSFR 111  
Db 278 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIILKDTSDSENSFR 328

RESULT 7  
US-09-935-727-9

; Sequence 9, Application US/09935727  
; Patent No. US20020150583A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
; FILE REFERENCE: PF454P2  
; CURRENT APPLICATION NUMBER: US/09/935,727  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/303,224  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: 60/252,131  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/227,598  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: 09/518,931  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/168,235  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 60/146,371  
; PRIOR FILING DATE: 1999-08-02  
; PRIOR APPLICATION NUMBER: 60/131,964  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/131,270  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/124,092  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/121,774  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: 09/006,352  
; PRIOR FILING DATE: 1998-01-13  
; PRIOR APPLICATION NUMBER: 60/035,496  
; PRIOR FILING DATE: 1997-01-14  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-727-9

Query Match 100.0%; Score 557; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 4.1e-51;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db 218 ETVAINLSVDLSKYITTIAGVMTLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
  
QY 61 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIILKDTSDSENSFR 111  
Db 278 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIILKDTSDSENSFR 328

RESULT 8  
US-09-314-889-6  
; Sequence 6, Application US/09314889  
; Publication No. US20030077694A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:

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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible.
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/314,889
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/815,469
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/028,711
/ FILING DATE: 17-OCT-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/013,285
/ FILING DATE: 12-MAR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Steffe, Eric K.
/ REGISTRATION NUMBER: 36,688
/ REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 335 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: protein
/ US-09-314-889-6

Query Match 100.0%; Score 557; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 4.1e-51;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60
DB 218 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277

QY 61 LRNWHQHGKKEAYDTLLKDLKANLCTLAETIILKDTITSDSENSNFR 111
DB 278 LRNWHQHGKKEAYDTLLKDLKANLCTLAETIILKDTITSDSENSNFR 328

RESULT 9
US-10-619-220-2
; Sequence 2, Application US/10619220
; Publication No. US20040033979A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/10/619,220
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 09/802,669
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
/ US-10-619-220-2

Query Match 100.0%; Score 557; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 4.1e-51;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60
DB 218 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277

QY 61 LRNWHQHGKKEAYDTLLKDLKANLCTLAETIILKDTITSDSENSNFR 111
DB 278 LRNWHQHGKKEAYDTLLKDLKANLCTLAETIILKDTITSDSENSNFR 328

RESULT 10
US-10-005-842-4
; Sequence 4, Application US/10005842
; Publication No. US20020098550A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Gentz, Reiner
; Yu, Guo-Liang
; Su, Jeffrey
; Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/005,842
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,583
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/040,846
; FILING DATE: 17-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF366
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3013098504
; TELEFAX: 3013098439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
/ US-10-005-842-4

Query Match 100.0%; Score 557; DB 13; Length 335;
Best Local Similarity 100.0%; Pred. No. 4.1e-51;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60
DB 218 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277

QY 61 LRNWHQHGKKEAYDTLLKDLKANLCTLAETIILKDTITSDSENSNFR 111
DB 278 LRNWHQHGKKEAYDTLLKDLKANLCTLAETIILKDTITSDSENSNFR 328
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Db 278 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIKDIITSDSENSNFR 328

## RESULT 11

US-10-175-902-3  
; Sequence 3, Application US/10175902  
; Publication No. US20030108516A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Pan, James G.  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dixit, Vishva M.  
; TITLE OF INVENTION: Death Domain Containing Receptor 4  
; FILE REFERENCE: 1488.130005  
; CURRENT APPLICATION NUMBER: US/10/175,902  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 09/565,918  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: US 60/132,922  
; PRIOR FILING DATE: 1999-05-06  
; PRIOR APPLICATION NUMBER: US 09/013,895  
; PRIOR FILING DATE: 1998-01-27  
; PRIOR APPLICATION NUMBER: US 60/037,829  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: US 60/035,722  
; PRIOR FILING DATE: 1997-01-28  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-175-902-3

Query Match 100.0%; Score 557; DB 14; Length 335;

Best Local Similarity 100.0%; Pred. No. 4.1e-51;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60

Db 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277

QY 61 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIKDIITSDSENSNFR 111

Db 278 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIKDIITSDSENSNFR 328

## RESULT 12

US-10-186-643-7  
; Sequence 7, Application US/10186643  
; Publication No. US20030118546A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: Ni, Jian  
; APPLICANT: Gentz, Reiner  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
; FILE REFERENCE: 1488.128004  
; CURRENT APPLICATION NUMBER: US/10/186,643  
; CURRENT FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: US/09/573,986  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-186-643-7

Query Match

Best Local Similarity 100.0%; Score 557; DB 14; Length 335;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60

Db 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277

QY 61 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIKDIITSDSENSNFR 111

Db 278 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIKDIITSDSENSNFR 328

## RESULT 13

US-10-189-189-6  
; Sequence 6, Application US/10189189  
; Publication No. US20030170203A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; FILE REFERENCE: 1488.031000C  
; CURRENT APPLICATION NUMBER: US/10/189,189  
; CURRENT FILING DATE: 2002-07-05  
; PRIOR APPLICATION NUMBER: US 60/314,314  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/303,155  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: US 09/557,908  
; PRIOR FILING DATE: 2000-04-21  
; PRIOR APPLICATION NUMBER: US 60/136,741  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 60/130,488  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 08/815,469  
; PRIOR FILING DATE: 1997-03-11  
; PRIOR APPLICATION NUMBER: US 60/037,341  
; PRIOR FILING DATE: 1997-02-06  
; PRIOR APPLICATION NUMBER: US 60/028,711  
; PRIOR FILING DATE: 1996-10-17  
; PRIOR APPLICATION NUMBER: US 60/013,285  
; PRIOR FILING DATE: 1996-03-12  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-189-189-6

Query Match 100.0%; Score 557; DB 14; Length 335;

Best Local Similarity 100.0%; Pred. No. 4.1e-51;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60

Db 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277

QY 61 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIKDIITSDSENSNFR 111

Db 278 LRNWHQLHGKKEAYDTLTKLKKANLCTLAETKIQTIIKDIITSDSENSNFR 328

## RESULT 14

US-10-418-242-9  
; Sequence 9, Application US/10418242  
; Publication No. US20040013664A1  
; GENERAL INFORMATION:  
; APPLICANT: Gentz et al.  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
; FILE REFERENCE: PF454P3  
; CURRENT APPLICATION NUMBER: US/10/418,242

```
/ CURRENT FILING DATE: 2003-04-18
/ PRIOR APPLICATION NUMBER: 60/373,604
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: 09/935,727
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: 60/303,224
/ PRIOR FILING DATE: 2001-07-06
/ PRIOR APPLICATION NUMBER: 60/252,131
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/227,598
/ PRIOR FILING DATE: 2000-08-25
/ PRIOR APPLICATION NUMBER: 09/518,931
/ PRIOR FILING DATE: 2000-03-03
/ PRIOR APPLICATION NUMBER: 60/168,235
/ PRIOR FILING DATE: 1999-12-01
/ PRIOR APPLICATION NUMBER: 60/146,371
/ PRIOR FILING DATE: 1999-08-02
/ PRIOR APPLICATION NUMBER: 60/131,964
/ PRIOR FILING DATE: 1999-04-30
/ PRIOR APPLICATION NUMBER: 60/131,279
/ PRIOR FILING DATE: 1999-04-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 51
/ SEQ ID NO 9
/ LENGTH: 335
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-418-242-9

Query Match      100.0%; Score 557; DB 15; Length 335;
Best Local Similarity 100.0%; Pred. No. 4.1e-51;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTABQKVL 60
Db 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTABQKVL 277

QY 61 LRNWHQHGKKEAYDTLLKDLKANLCTLAETIAEKIQTIIILKDTSDSENSNFR 111
Db 278 LRNWHQHGKKEAYDTLLKDLKANLCTLAETIAEKIQTIIILKDTSDSENSNFR 328

RESULT 15
US-10-226-296-3
/ Sequence 3, Application US/10226296
/ Publication No. US20030036168A1
/ GENERAL INFORMATION:
/ APPLICANT: Ni, Jian
/ Rosen, Craig A.
/ Pan, James G.
/ Gentz, Reiner L.
/ Dixit, Vishva M.
/ TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
/ Receptor 4), Member of the TNF-Receptor
/ Superfamily and Binding to Trail (AP02-L)
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: HUMAN GENOME SCIENCES, INC.
/ STREET: 9410 KEY WEST AVENUE
/ CITY: ROCKVILLE
/ STATE: MD
/ COUNTRY: US
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA: US/10/226,296
/ APPLICATION NUMBER: US/10/226,296
/ FILING DATE: 23-Aug-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US/09/448,868
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: 09/013,895
/ FILING DATE: 27-JAN-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: STEFFE, ERIC K.
/ REGISTRATION NUMBER: 36,688
/ REFERENCE/DOCKET NUMBER: 1488.1300004
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 669 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-226-296-3

Query Match      100.0%; Score 557; DB 14; Length 669;
Best Local Similarity 100.0%; Pred. No. 1e-50;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTABQKVL 60
Db 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTABQKVL 277

QY 61 LRNWHQHGKKEAYDTLLKDLKANLCTLAETIAEKIQTIIILKDTSDSENSNFR 111
Db 278 LRNWHQHGKKEAYDTLLKDLKANLCTLAETIAEKIQTIIILKDTSDSENSNFR 328

Search completed: June 1, 2004, 14:50:04
Job time : 35.8922 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:37:07 ; Search time 11.6317 Seconds  
(without alignments)  
917.942 Million cell updates/sec

Title: US-09-854-906-9

Perfect score: 557

Sequence: 1 ETVAINLSVDLSKVITTTIA.....KIQTIIKIDITSSENSNFR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PTR 78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	557	100.0	314	2 I37383	FAS soluble protei
2	557	100.0	335	2 A40036	apoptosis-mediati
3	278.5	50.0	327	2 A46484	apoptosis-mediati
4	250.5	45.0	324	2 JC2395	Fas antigen precu
5	86.5	15.5	1979	2 C71622	hypothetical prote
6	81.5	14.6	589	2 C97241	methyl-accepting c
7	80.5	14.5	656	2 I49299	receptor interacti
8	78.5	14.1	671	2 T09479	serine/threonine p
9	78.5	14.1	4196	2 T43274	dynein heavy chain
10	77.5	13.9	416	2 A45105	farnesyl-diphospha
11	77.5	13.9	1558	2 B71603	RESA-H3 antigen p
12	76.5	13.7	275	2 S40903	FUN4 protein - yea
13	76	13.6	406	2 I39332	replication protei
14	76	13.6	640	2 AE1895	hypothetical prote
15	75.5	13.6	285	2 I41162	DNA-binding protei
16	75	13.5	261	2 S14875	dnak-type molecula
17	75	13.5	265	2 A31457	rns protein - Esch
18	75	13.5	671	2 D72346	chemotaxis sensor
19	74	13.3	106	2 D86641	transcription regu
20	74	13.3	191	2 H71045	hypothetical prote
21	74	13.3	548	2 G97047	single-stranded-DN
22	74	13.3	575	2 S46692	hypothetical prote
23	73.5	13.2	365	2 C70116	recombination prot
24	73.5	13.2	395	2 T50804	hypothetical prote
25	73.5	13.2	643	2 B71848	probable outer mem
26	73	13.1	227	2 G70182	hypothetical prote
27	73	13.1	371	2 T21819	hypothetical prote
28	73	13.1	461	2 JC4302	tumor necrosis fac
29	73	13.1	552	2 T04653	receiver-like prot

ALIGNMENTS

RESULT 1

I37383

FAS soluble protein - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 07-Jul-2003

C:Accession: I37383

R:Cascino, I.; Ficuci, G.; Papoff, G.; Ruberti, G.

J. Immunol. 154, 2706-2713, 1995

A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are

A;Reference number: I37383; MUID:95181785; PMID:7533181

A;Accession: I37383

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-314 <RES>

A;Cross-references: EMBL:Z47993; NID:G728578; PIDN:CAA89031.1; PID:G695539

C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 100.0%; Score 557; DB 2; Length 314;

Best Local Similarity 100.0%; Pred. No. 7,1e-41;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKVITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
|||||  
Db 197 ETVAINLSVDLSKVITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 256

QY 61 LRNWHOLHGKKEAYDTLLKDLKANLCTLAETKIQTIIKIDITSSENSNFR 111  
|||||

Db 257 LRNWHOLHGKKEAYDTLLKDLKANLCTLAETKIQTIIKIDITSSENSNFR 307  
|||||

RESULT 2

A40036

apoptosis-mediating surface antigen Fas precursor - human

N;Alternate names: surface antigen APO-1

C:Species: Homo sapiens (man)

C>Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 07-Jul-2003

C:Accession: A40036; S24543; A38142

R;Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase,

Cell 66, 233-243, 1991

A;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can medi

A;Reference number: A40036; MUID:91309137; PMID:1713127

A;Accession: A40036

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-335 <ITO>

A;Cross-references: GB:M67454; NID:G182409; PIDN:AAA63174.1; PID:G182410

R;Kramer, P.H.

submitted to the EMBL Data Library, February 1992

A;Reference number: S24543

A;Accession: S24543

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-335 <KRA>  
A;Cross-references: ENBL:X63717; NID:G28741; PID:G28742  
J;Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Mater, G.; Klas, C.; Li-Weber, M.; Rich  
J. Biol. Chem. 267, 10709-10715, 1992  
A;Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member  
A;Reference number: A38142; MUID:92268122; PMID:1375228  
A;Accession: A38142  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-134, 'Q', 136-335 <OE>  
A;Experimental source: SKW6.4 cells  
A;Note: sequence extracted from NCBI backbone (NCBIP:103810)  
A;Note: in NCBI backbone the source is designated as mouse  
C;Genetics:  
A;Gene: GDB:APT1  
A;Cross-references: GDB:132671; OMIM:134637  
A;Map position: 10q24.1-10q24.1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: apoptosis; surface antigen; transmembrane protein  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;85-128/Domain: NGF receptor repeat homology <NG4>  
F;174-190/Domain: transmembrane #status predicted <TMM>  
Query Match 100.0%; Score 557; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 7.6e-41;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ETVAIINLSDVLSKYITTTAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
DB 218 ETVAIINLSDVLSKYITTTAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277  
QY 61 LRNWHQHGKKEAYDTLLIKLKKANLCTLAETKIQITLLKX---ITSSENSN 109  
DB 278 LRNWHQHGKKEAYDTLLIKLKKANLCTLAETKIQITLLKX---ITSSENSN 328  
RESULT 3  
A46484  
apoptosis-mediating membrane-associated polypeptide Fas - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Jul-2003  
C;Accession: A46484; A47254  
R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins,  
J. Immunol. 148, 1274-1279, 1992  
A;Title: The CDNA structure, expression, and chromosomal assignment of the mouse Fas and  
A;Reference number: A46484; MUID:92148151; PMID:1371136  
A;Accession: A46484  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-327 <WAT>  
A;Cross-references: GB:M83649; NID:G193225; PIDN:AAA37593.1; PID:G193226  
A;Experimental source: BAMS macrophage cell line  
A;Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)  
R;Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.  
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
A;Title: Aberrant transcription caused by the insertion of an early transposable element  
A;Reference number: A47254; MUID:93189576; PMID:7680478  
A;Accession: A47254  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-96 <ADA>  
A;Cross-references: GB:S56490; NID:G298505; PIDN:AAB25700.1; PID:G298506  
A;Experimental source: MRL lpr/lpr  
A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126863, NCBIN:126863,  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: transmembrane protein  
F;44-79/Domain: NGF receptor repeat homology <NG4>  
F;81-124/Domain: transmembrane #status predicted <TMM>  
Query Match 50.0%; Score 278.5; DB 2; Length 327;  
Best Local Similarity 50.9%; Pred. No. 8.5e-17;  
Matches 57; Conservative 18; Mismatches 34; Indels 3; Gaps 1;

QY 1 ETVAIINLSDVLSKYITTTAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
DB 210 ETIPWNASNLSSKYIPRIABDMTIQEAKKFARENNIKEGKIDIMHDSIQDTAEQKVL 269  
QY 61 LRNWHQHGKKEAYDTLLIKLKKANLCTLAETKIQITLLKDI---TSSENSN 109  
DB 270 LLCWYQSHGKSDAYQDLIKGLKKAECRRTLDFQDMVQKDLGKSTPFDGTGNN 321  
RESULT 4  
JC2395  
Fas antigen precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-Jul-2003  
C;Accession: JC2395; PC2246  
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.  
Biochem. Biophys. Res. Commun. 198, 666-674, 1994  
A;Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liv  
A;Reference number: JC2395; MUID:94128114; PMID:7507668  
A;Accession: JC2395  
A;Molecule type: mRNA  
A;Residues: 1-324 <KIM>  
A;Cross-references: DDBJ:D26112; NID:G468486; PIDN:BAA05108.1; PID:di005650; PID:G46848  
A;Experimental source: thymus  
A;Accession: PC2246  
A;Molecule type: mRNA  
A;Residues: 1-62, 'RFT', <KIT>  
A;Cross-references: DDBJ:D26113; NID:G468488; PIDN:BAA05109.1; PID:di005651; PID:G46848  
A;Experimental source: liver  
C;Genetics:  
A;Introns: G2/1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-324/Product: Fas antigen #status predicted <WAT>  
F;44-79/Domain: NGF receptor repeat homology <NGF>  
F;81-124/Domain: NGF receptor repeat homology <NG4>  
F;171-188/Domain: transmembrane #status predicted <TMM>  
Query Match 45.0%; Score 250.5; DB 2; Length 324;  
Best Local Similarity 46.4%; Pred. No. 2.2e-14;  
Matches 52; Conservative 25; Mismatches 32; Indels 3; Gaps 1;  
QY 1 ETVAIINLSDVLSKYITTTAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
DB 207 ESVPMNVSDVNLKIMRTAEKMKICDAKKFARQHKIPESKIDIEHNSPDAAEQKIQ 266  
QY 61 LRNWHQHGKKEAYDTLLIKLKKANLCTLAETKIQITLLKX---ITSSENSN 109  
DB 267 LQWYQSHGKTGACQALIQGLRKANCRDIAEIQAMVWEDHENSISNSRNN 318  
RESULT 5  
C71622  
hypothetical protein PFB0145c - malaria parasite (Plasmodium falciparum)  
C;Species: Plasmodium falciparum  
C;Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 21-Jul-2000  
C;Accession: C71622  
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.  
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.  
Science 282, 1126-1132, 1998  
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A;Reference number: A71600; MUID:99021743; PMID:9804551  
A;Accession: C71622  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1979 <GAR>  
A;Cross-references: GB:AE001375; GB:AE001362; NID:G3845105; PIDN:AACT71819.1; PID:G38451  
A;Experimental source: clone 3D7  
A;Gene: PFB0145c  
Query Match 15.5%; Score 86.5; DB 2; Length 1979;

Best Local Similarity 23.0%; Pred. No. 23;  
Matches 35; Conservative 32; Mismatches 40; Indels 45; Gaps 7;  
Query Match 14.6%; Score 81.5; DB 2; Length 589;  
Best Local Similarity 24.0%; Pred. No. 17;  
Matches 29; Conservative 30; Mismatches 39; Indels 23; Gaps 6;  
Query 5 INLSVDLSKVITTIAG-----VMTLSQVKGVRKNGVN-----EAKIDEIKNDNVQDTAE 55  
Db 307 LSSSTEVEKVISVSSGASSQVSDLSISGLLANFNDNISIIYSKLEQVKNEG--DAAN 364  
Query 56 QKV-----QLLRNWHQHGKAEYDVLTKLKNANLCTLAETII--LKDITSDSENS 108  
Db 365 SKISSGESELTFLNSMTWKETFEVVKIQALN-----ESINEIINTTKFINEISEDT 419  
Query 109 N 109  
Db 420 N 420  
RESULT 7  
I49299  
receptor interacting protein RIP - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 05-Nov-1999  
C:Accession: I49299  
R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.  
Cell 81, 513-523, 1995  
A:Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1 (C  
A:Reference number: A56913; MUID:95277838; PMID:7538908  
A:Accession: I49299  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-656 <RES>  
A:Cross-references: EMBL:U25995; NID:9829618; PIDN:RAB60487.1; PID:9829619  
C:Genetics:  
A:Gene: RIP  
C:Superfamily: protein kinase homology  
F:15-293/Domain: protein kinase homology <KIN>

Query Match 14.5%; Score 80.5; DB 2; Length 656;  
Best Local Similarity 41.7%; Pred. No. 23;  
Matches 20; Conservative 8; Mismatches 19; Indels 1; Gaps 1;  
Query 27 QVKGVRKNGVNEAKIDEIKNDNVQDTAEQKV-QLLRNWHQHLHGKKEA 73  
Db 582 QWKNCAKLGFTSQIDEIDHDYERDGLKRVYQMLQKWLMEGTGKA 629  
RESULT 8  
T09479  
serine/threonine protein kinase (EC 2.7.1.1-) RIP - human  
C:Species: Homo sapiens (man)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 17-Nov-2000  
C:Accession: T09479; I38992  
R:Huang, J.; Hsu, H.; Baichwal, V.R.; Goeddel, D.V.  
submitted to the EMBL Data Library, August 1998  
A:Reference number: Z16685  
A:Accession: T09479  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-671 <HUA>  
A:Cross-references: EMBL:U50062; NID:93426026; PID:93426027  
R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.  
Cell 81, 513-523, 1995  
A:Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1 (C  
A:Reference number: A56913; MUID:95277838; PMID:7538908  
A:Accession: I38992  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 300-513, S', 515-671 <RES>  
A:Cross-references: EMBL:U25994; NID:9829616; PIDN:AAC50137.1; PID:9829617  
C:Genetics:  
A:Gene: RIP  
C:Keywords: ATP binding; phosphotransferase

Query Match 14.1%; Score 78.5; DB 2; Length 671;  
Best Local Similarity 31.4%; Pred. No. 35;  
Matches 22; Conservative 17; Mismatches 28; Indels 3; Gaps 2;  
Query 29 KGFRKNGVNEAKIDEIKNDNVQDTAEQKV-QLLRNWHQHLHGKKEAYDTTLKOLKKNLC 87  
Db 599 KNCARKLGFTSQIDEIDHDYERDGLKRVYQMLQKWLMEGTGKA--TVGKLAQALHQC 656  
Query 88 TLAEKIQTII 97  
Db 657 SRIDLSSLI 666  
RESULT 9  
T43274  
dynein heavy chain, cytosolic - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T43274  
R:Yamamoto, A.; West, R.R.; McIntosh, J.R.; Hiraoka, Y.  
J. Cell Biol. 145, 1233-1250, 1999  
A:Title: A cytoplasmic dynein heavy chain is required for oscillatory nuclear movement c  
A:Reference number: 223893; MUID:95296615; PMID:10366596  
A:Accession: T43274  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-4196 <YAM>  
A:Cross-references: EMBL:AB006784; NID:92351080; PIDN:BAA22056.1; PID:92351081  
A:Experimental source: strain CRL152  
C:Genetics:  
A:Gene: dhcl  
A:Map position: 1  
C:Superfamily: dynein heavy chain, cytosolic  
Query Match 14.1%; Score 78.5; DB 2; Length 4196;  
Best Local Similarity 23.0%; Pred. No. 2.5e+02;  
Matches 29; Conservative 29; Mismatches 47; Indels 21; Gaps 3;

QY 4 AINLSVDLSKYITTIAGVNTLS--QVKGVR-----KNGVNEAKIDEIKN 47  
 Db 410 ALSLSNVDFSHRTAVSGDILSLCVIRKDFLRISGLKEEQSYGLKNSIKQIKAFENKL 469  
 QY 48 DNVQDTRAQVKQLLRNWHQHG-----KKEAYDTLTKDLKKNLCVLAELKIQTIIILKDT 102  
 Db 470 KYIQSFHEKQQLIGALSEVYGLTHTLLEILHLNKAKEHVFNLITVFKDLSLNVLDIS 529  
 QY 103 SDSENS 108  
 Db 530 LKGVNA 535  
 RESULT 10  
 A45105  
 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - rat  
 N;Alternate names: squalene synthase  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Jun-1999  
 C;Accession: A45105  
 R;McKenzie, T.L.; Jiang, G.; Straubhaar, J.R.; Conrad, D.G.; Shechter, I.  
 J. Biol. Chem. 267, 21368-21374, 1992  
 A;Title: Molecular cloning, expression, and characterization of the cDNA for the rat hep  
 A;Reference number: A45105; MUID:93016074; PMID:14000448  
 A;Accession: A45105  
 A;Status: preliminary  
 A;Molecule type: mRNA; protein  
 A;Residues: 1-416 <MCK>  
 A;Cross-references: GB:M95591; NID:g207070; PIDN:AAA42179.1; PID:g207071  
 A;Experimental source: hepatoma cell line H35  
 A;Note: sequence extracted from NCBI backbone (NCBIN:116694, NCBIPI:116696)  
 C;Superfamily: farnesyl-diphosphate farnesyltransferase  
 C;Keywords: transferase; transmembrane protein  
 Query Match 13.9%; Score 77.5; DB 2; Length 416;  
 Best Local Similarity 28.4%; Pred.No.26;  
 Matches 25; Conservative 14; Mismatches 20; Indels 29; Gaps 4;  
 QY 48 DNVQD---TAEQKVQLLRNWH-----QLHGKKEAYDTLTKDLKKNL--CTLAEKI 93  
 Db 80 DTVEDDMAISVEKKIPLRNFHFLYEPFWRFTSEKSHRVLEDPFTISLEFRNLAEKY 139  
 QY 94 QTIIL-----KDITSDSE 106  
 Db 140 QTVIADICHRMCGGAAFFLNKDVTSKOD 167  
 RESULT 11.  
 B71603  
 RESA-H3 antigen PFB0915w - malaria parasite (Plasmodium falciparum)  
 C;Species: Plasmodium falciparum  
 C;Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 21-Jul-2000  
 C;Accession: B71603  
 R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, E.V.;  
 ; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.  
 Science 282, 1126-1132, 1998  
 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
 A;Reference number: A71600; MUID:99021743; PMID:9804551  
 A;Accession: B71603  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-1558 <GAR>  
 A;Cross-references: GB:AE001424; GB:AE001362; NID:g3845307; PIDN:AACT1972.1; PID:g3845307  
 A;Experimental source: clone 3D7  
 C;Genetics:  
 A;Gene: PFB0915w  
 Query Match 13.9%; Score 77.5; DB 2; Length 1558;  
 Best Local Similarity 23.1%; Pred.No.1.1e+02;  
 Matches 36; Conservative 23; Mismatches 42; Indels 55; Gaps 6;  
 QY 1 ETVAINLSVDLSKYI-----TTIAGVNTLSQ 27

```

Db      585 ENVATNLSNDLLSNLGGITEETKOSILNEIEVKENVVVTTILENVETTAESVTTSN   644
          ||| |||| |:: : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      28 VKGFVRKNGVN---EAKIDEIKNDNQDTAEQKVQLRNWHOLHGKKEAYDTLIKDLKK   83
          ::::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:::
Db      645 ILREIQENTINDRIEEKLEEL-HENVLAA-----LENTQSEEEKKEVID-VIEEVKE   696
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      84 ANLCITLAEKIQ-----TIILKOITSSENSN 109
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      697 EVATTIETVEQAEBESASTITEIFENLEENAVESN 732
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
FUN403
FUN4 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YAR008w
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Oct-1999
C;Accession: S40903
R;Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Fortin, N.; Zeng, B.; Delaney, S.; Ou
submitted to the EMBL Data Library, November 1993
A;Description: Sequencing of chromosome I of Saccharomyces cerevisiae: Analysis of the
A;Reference number: S40891
A;Accession: S40903
A;Molecule type: DNA
A;Residues: 1-275 <CIA>
A;Cross-references: EMBL:L22015; NID:g1339990; PIDN:AAC04961.1; PID:g349753; MIPS:YAR00
C;Genetics:
A;Gene: SGD:SEN34; FUN4
A;Cross-references: MIPS:YAR008w; SGD:S0000066
A;Map position: LR

Query Match      13.7%; Score 76.5; DB 2; Length 275;
Best Local Similarity 24.0%; Pred. No. 20;
Matches 31; Conservative 24; Mismatches 33; Indels 41; Gaps 5;

Qy      7 LSDVDLSKYITIAGWTLSQ-----VGKFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLL 61
          ||| ||| :: : ||| ||| :: : ||| ||| :: : ||| ||| :: : ||| |||
Db      45 LEDV-LWLHLNLADVKLIROEGDEIMEGITLERG---AKLSKIYNDRLNKSF----- 94
          ||| ||| :: : ||| ||| :: : ||| ||| :: : ||| ||| :: : ||| |||
Qy      62 RNWHOLHGKKEAYDTLIKDLKANCLTAEKIQ-----TTIL 98
          ::| ||| ::| ||| ::| ||| ::| ||| ::| ||| ::| ||| ::| |||
Db      95 ---YORFKFDEHIAKIKIGRIDNKTABEQRLDKSSNNDDLISSLFDIANTSMIL 151
          ::| ||| ::| ||| ::| ||| ::| ||| ::| ||| ::| ||| ::| |||
Qy      99 KDITSDSEN 107
          ::| ||| ||| ::|
Db      152 RDIRSDDS 160

RESULT 13
I39932
replication protein ori60 - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 15-Oct-1999
C;Accession: I39932
R;Baum, J.A.; Gilbert, M.P.
J. Bacteriol. 173, 5280-5289, 1991
A;Title: Characterization and comparative sequence analysis of replication origins from
A;Reference number: I39930; MUID:91358302; PMID:1885511
A;Accession: I39932
A;Status: preliminary; translated from GB/EMBL/DDBB
A;Molecule type: DNA
A;Residues: 1-406 <RES>
A;Cross-references: GB:M60475; NID:g143276; PIDN:AAA22634.1; PID:g143277
C;Genetics:
A;Gene: ori60

Query Match      13.6%; Score 76; DB 2; Length 406;
Best Local Similarity 28.8%; Pred. No. 34;
Matches 30; Conservative 24; Mismatches 36; Indels 14; Gaps 6;

Qy      7 LSDVDLSKYITIAGWMT--LSQ-VGKFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLN 63
          ::| ||| ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed: June 1, 2004, 14:47:10  
Job time : 13.6317 secs

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Db 251 ISDMKTDKYIATIKGHIKKWVSQMSFSDIENVEQAYLEERKQLQ-KPKSQQKPNSLK- 308
QY 64 WHQLHGKKEAYDTLTKDLKKAANCTLAETKIQTLITLSDSEN 107
Db 309 --PSYGGKDIVPEWLKEQKLD-----EVQT--NKELHONSES 343

RESULT 14
AEI1895
hypothetical protein all0711 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AE1895
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE1895
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-640 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAE72668.1; PID:g17130056; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all0711

Query Match 13.6%; Score 76; DB 2; Length 640;
Best Local Similarity 26.8%; Pred. No. 55;
Matches 22; Conservative 18; Mismatches 36; Indels 6; Gaps 2;

QY 17 TTIAGVWTLTSGVGRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNWHQLHGKKEAYDT 76
Db 562 TVEAKTNVNFPSWRSSFNDRKIDICK-QVNELEKVIQ-----EQLTANQDAFDK 615

QY 77 LIRDLKKAANCTLAETKIQTL 98
Db 616 LISKVEGLQKALSTKVQEAII 637

RESULT 15
I41162
DNA-binding protein cafD - Escherichia coli
C:Species: Escherichia coli
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 26-Aug-1999
C:Accession: I41162
R;Savelkoul, P.H.; Willshaw, G.A.; McConnell, M.M.; Smith, H.R.; Hamers, A.M.; van der Z
Microb. Pathog. 8, 91-99, 1990
A:Title: Expression of CFA/I fimbriae is positively regulated.
A:Reference number: I41162; MUID:90271755; PMID:1971911
A:Accession: I41162
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-265 <RES>
A:Cross-references: GB:M55609; NID:g145505; PIDN:AAA62773.1; PID:g145506
C:Genetics:
A:Gene: cfad
C:Superfamily: fapR protein

Query Match 13.6%; Score 75.5; DB 2; Length 265;
Best Local Similarity 23.4%; Pred. No. 23;
Matches 25; Conservative 22; Mismatches 31; Indels 29; Gaps 3;

QY 29 KGFVRK---NGVNEAKIDEIKNDNVQDTAEQKVOLLRNWHQLHGKKEAYDTLIKDKKAN 85
Db 103 RGMRSKIMTTEVNTKLLDELKNINSHDDSAFISSLI----YLSKIENNEKIESIYISS 158

QY 86 LCTLAETKIQTLITLSDSEN 110
Db 159 VSFFSKVRNVIEKLSRKWTGLIADAFNVSEITIRKLESENTNF 205
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:33:56 ; Search time 7.97605 Seconds  
(without alignments)  
724.643 Million cell updates/sec

Title: US-09-854-906-9

Perfect score: 557

Sequence: 1 ETVAINLSDVLSKYITTTA.....KIQTIIILKDIITSDSENSFR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	100.0	335	1	TNR6 HUMAN
2	337	60.5	332	1	TNR6_PIG
3	331	59.4	323	1	TNR6_BOVIN
4	278.5	50.0	327	1	TNR6_MOUSE
5	250.5	45.0	324	1	TNR6_RAT
6	81	14.5	657	1	THO1_MOUSE
7	80.5	14.5	656	1	R1K1_MOUSE
8	78.5	14.1	343	1	THO1_RAT
9	78.5	14.1	671	1	R1K1_HUMAN
10	78.5	14.1	4196	1	DYHC SCHPO
11	77.5	13.9	416	1	FDFT RAT
12	76.5	13.7	275	1	SE34 YEAST
13	75.5	13.6	265	1	CFAD_ECOLI
14	75	13.5	265	1	RNS_ECOLI
15	75	13.5	671	1	CHEA_THEMA
16	74	13.3	575	1	YHZE YEAST
17	74	13.3	743	1	FTSK_CLOTE
18	73.5	13.2	365	1	RECA_BORBU
19	73	13.1	461	1	TE1A_PIG
20	73	13.1	471	1	TR1A_BOVIN
21	73	13.1	508	1	KLC DROME
22	73	13.1	552	1	ARRA_ARATH
23	73	13.1	657	1	THO1_HUMAN
24	73	13.1	1169	1	SMC_METUA
25	73	13.1	1175	1	P1B4_HUMAN
26	72	12.9	700	1	VO18_FOPFV
27	72	12.9	879	1	RA50_SULTO
28	72	12.9	1175	1	P1B4_RAT
29	72	12.9	1355	1	DP3A_SYNV3
30	71.5	12.8	320	1	MCAE_CAMTE
31	71.5	12.8	1044	1	YAF3_SCHPO
32	71.5	12.8	1075	1	Y124_METUA
33	71	12.7	205	1	FADD_MOUSE

## RESULT 1

ID	TNR6 HUMAN	STANDARD;	PRT;	335 AA.
AC	P25445; Q14293; Q14294; Q14295; Q16652;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).			
DE	TNFRSF6 OR APT1 OR FAS OR FASL.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=91309137; PubMed=1713127;			
RA	Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I., Sameshima M., Hase A., Seto Y., Nagata S.;			
RA	"The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis.";			
RT	Cell 66:233-243(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 226-240; 269-291 AND 321-335.			
RX	MEDLINE=92268122; PubMed=1375228;			
RA	Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C., Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H., Krammer P.H.;			
RA	"Purification and molecular cloning of the APO-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth factor receptor superfamily. Sequence identity with the Fas antigen.";			
RT	J. Biol. Chem. 267:10709-10715(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 6), AND FUNCTION.			
RX	MEDLINE=95181785; PubMed=7533181;			
RA	Cascino I., Fiucci G., Papoff G., Ruberti G.;			
RA	"Three functional soluble forms of the human apoptosis-inducing Fas molecule are produced by alternative splicing.";			
RT	J. Immunol. 154:2706-2713(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 5).			
RC	TISSUE=Peripheral blood lymphocytes;			
RA	Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;			
RA	Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).			
RX	MEDLINE=96238926; PubMed=8648105;			
RA	Papoff G., Cascino I., Sramo A., Starace G., Lynch D.H., Ruberti G.;			
RA	"An N-terminal domain shared by Fas/Apo-1 (CD95) soluble variants prevents cell death in vitro.";			
RT	J. Immunol. 156:4622-4630(1996).			
RN	[6]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Urinary bladder;			

Q92jff4 rickettsia  
Q57959 methanococc  
P55737 arabidopsis  
P51818 arabidopsis  
P22516 saccharomyc  
Q81vf6 homo sapien  
Q931k4 staphylococ  
Q998g9 anopheles g  
P35039 anopheles g  
Q03001 homo sapien  
Q8d305 wiggleswort  
Q9v1h5 pyrococcus

## ALIGNMENTS

- RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettner K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [7]  
RP INTERACTION WITH RIPK1.  
RX MEDLINE=95277838; PubMed=7538908;  
RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;  
RT "RIP: a novel protein containing a death domain that interacts with  
RT Fas/APO-1 (CD95) in yeast and causes cell death.";  
RL Cell 81:513-523(1995).  
RN [8]  
RP INTERACTION WITH FAIM2.  
RX MEDLINE=2006292; PubMed=10535980;  
RA Somla N.V., Schmitt M.J., Vetter D.E., Van Antwerp D., Heinemann S.F.,  
RA Verma I.M.;  
RT "LFG: an anti-apoptotic gene that provides protection from fas-  
RT mediated cell death.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:12667-12672(1999).  
RN [9]  
RP STRUCTURE BY NMR OF 218-335.  
RX MEDLINE=97122332; PubMed=8967952;  
RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;  
RT "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";  
RL Nature 384:638-641(1996).  
RN [10]  
RP VARIANT ALPS PRO-241.  
RX MEDLINE=95300225; PubMed=7540117;  
RA Fisher G.H., Rosenberg F.J., Straus S.E., Dale J.K., Middleton L.A.,  
RA Lin A.Y., Strober W., Lenardo M.J., Puck J.M.;  
RT "Dominant interfering Fas gene mutations impair apoptosis in a human  
RT autoimmune lymphoproliferative syndrome.";  
RL Cell 81:935-946(1995).  
RN [11]  
RP VARIANT ALPS TYR-260.  
RX MEDLINE=97066823; PubMed=8929361;  
RA Drappa J., Vaishnaw A.K., Sullivan K.E., Chu J.-L., Elkon K.B.;  
RT "Fas gene mutations in the Canale-Smith syndrome, an inherited  
RT lymphoproliferative disorder associated with autoimmunity.";  
RL New Engl. J. Med. 335:1643-1649(1996).  
RN [12]  
RP VARIANTS ALPS TRP-121 AND CYS-232.  
RX MEDLINE=97180145; PubMed=9028321;  
RA Bettinardi A., Brugnani D., Quiros-Roldan E., Malagoli A.,  
RA La Grutta S., Correria A., Notarangelo L.D.;  
RT "Missense mutations in the Fas gene resulting in autoimmune  
RT lymphoproliferative syndrome: a molecular and immunological  
RT analysis.";  
RL Blood 89:902-909(1997).  
RN [13]  
RP VARIANTS ALPS ASP-257 AND SER-310.  
RX MEDLINE=97180739; PubMed=9028957;  
RA Sneller M.C., Wang J., Dale J.K., Strober W., Middleton L.A., Choi Y.,  
RA Fleisher T.A., Lim M.S., Jaffe E.S., Puck J.M., Lenardo M.J.,  
RA Straus S.E.;  
RT "Clincial, immunologic, and genetic features of an autoimmune  
RT lymphoproliferative syndrome associated with abnormal lymphocyte  
RT apoptosis.";  
RL Blood 89:1341-1348(1997).  
RN [14]  
RP VARIANT ALPS ALA-28.  
RX MEDLINE=97463833; PubMed=9322534;  
RA Pensati L., Costanzo A., Ianni A., Accapezzato D., Iorio R.,  
RA Natoli G., Nisini R., Almerighi C., Balsano C., Vajro P., Vegnente A.,  
RA Levero M.;  
RT "Fas/Apol mutations and autoimmune lymphoproliferative syndrome in a  
RT patient with type 2 autoimmune hepatitis.";  
RL Gastroenterology 113:1384-1389(1997).  
RN [15]  
RP VARIANT ALPS VAL-260.  
RX MEDLINE=99038860; PubMed=9821419;  
RA Infante A.J., Britton H.A., DeNapoli T., Middleton L.A., Lenardo M.J.,  
RA Jackson C.E., Wang J., Fleisher T., Straus S.E., Puck J.M.;  
RT "The clinical spectrum in a large kindred with autoimmune  
RT lymphoproliferative syndrome caused by a Fas mutation that impairs  
RT lymphocyte apoptosis.";  
RL J. Pediatr. 133:629-633(1998).  
RN [16]  
RP VARIANTS ALPS LYS-241 AND GLN-250.  
RX MEDLINE=99192346; PubMed=10090885;  
RA Jackson C.E., Fischer R.E., Hsu A.P., Anderson S.M., Choi Y., Wang J.,  
RA Dale J.K., Fleisher T.A., Middleton L.A., Sneller M.C., Lenardo M.J.,  
RA Straus S.E., Puck J.M.;  
RT "Autoimmune lymphoproliferative syndrome with defective Fas: genotype  
RT influences penetrance.";  
RL Am. J. Hum. Genet. 64:1002-1014(1999).  
RN [17]  
RP VARIANT ALPS GLY-272.  
RX MEDLINE=99270228; PubMed=10340403;  
RA Peters A.M., Kohfink B., Martin H., Griesinger F., Wormann B.,  
RA Gahr M., Roesler J.;  
RT "Defective apoptosis due to a point mutation in the death domain of  
RT CD95 associated with autoimmune lymphoproliferative syndrome, T-cell  
RT lymphoma, and Hodgkin's disease.";  
RL Exp. Hematol. 27:868-874(1999).  
RN [18]  
RP VARIANTS ALPS ARG-82; PRO-250; GLY-260 AND ILE-270.  
RX MEDLINE=99126461; PubMed=9927496;  
RA Vaishnaw A.K., Orlicki J.R., Chu J.-L., Krammer P.H., Chao M.V.,  
RA Elkon K.B.;  
RT "The molecular basis for apoptotic defects in patients with CD95  
RT (Fas/Apo-1) mutations.";  
RL J. Clin. Invest. 103:355-363(1999).  
RN [19]  
RP VARIANTS NON-HODGKIN'S LYMPHOMA THR-25; PHE-180; LEU-198;  
RX VAL-260; LYS-264; LYS-272; PHE-278 AND ASN-299.  
RX MEDLINE=99005325; PubMed=9787134;  
RA Groenbaek K., Straten P.T., Ralfkiaer E., Ahrenkiel V., Andersen M.K.,  
RA Hansen N.E., Zeuthen J., Hou-Jensen K., Guldberg P.;  
RT "Somatic Fas mutations in non-Hodgkin's lymphoma: association with  
RT extranodal disease and autoimmunity.";  
RL Blood 92:3018-3024(1998).  
RN [20]  
RP VARIANTS ALPS PRO-241; VAL-260; ILE-270 AND GLY-272.  
RX MEDLINE=21311411; PubMed=11418480;  
RA Straus S.E., Jaffe E.S., Puck J.M., Dale J.K., Elkon K.B.,  
RA Roosen-Wolf A., Peters A.M.J., Sneller M.C., Hallahan C.W., Wang J.,  
RA Fischer R.E., Jackson C.M., Lin A.Y., Baumler C., Siegfert E.,  
RA Marx A., Vaishnaw A.K., Grodzicky T., Fleisher T.A., Lenardo M.J.;  
RT "The development of lymphomas in families with autoimmune  
RT lymphoproliferative syndrome with germline Fas mutations and  
RT defective lymphocyte apoptosis.";  
RL Blood 98:194-200(2001).  
RN [21]  
RP FUNCTION: Receptor for TNFSF6/FASL. The adapter molecule FADD  
CC recruits caspase-8 to the activated receptor. The resulting death-  
CC inducing signaling complex (DISC) performs caspase-8 proteolytic  
CC activation which initiates the subsequent cascade of caspases  
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-  
CC mediated apoptosis may have a role in the induction of peripheral

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Query Match 100.0%; Score 557; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-41; 0; Indels 0; Gaps 0;
Matches 111; Conservative 0; Mismatches 0;

QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60
Db 218 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 277

QY 61 LRNWHOLHGKKEAYDPLIKDLKKNICTLAETKIQTIIILDKITSDSENFR 111
Db 278 LRNWHOLHGKKEAYDPLIKDLKKNICTLAETKIQTIIILDKITSDSENFR 328

RESULT 2
ID TNR6_PIG STANDARD; PRT; 332 AA.
AC 077736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
RT myocardium of pig."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ001202; CAA04596.1; -.
DR HSP; P25445; IDDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT SIGNAL 16 POTENTIAL.
```

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CHAIN 17 332 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 17 175 SUPERFAMILY MEMBER 6.
FT TRANSMEM 176 192 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 193 332 POTENTIAL.
FT REPEAT 45 81 CYTOPLASMIC (POTENTIAL).
FT REPEAT 82 125 TNFR-CYS 1.
FT REPEAT 126 164 TNFR-CYS 2.
FT DOMAIN 227 311 TNFR-CYS 3.
FT DISULFID 46 57 DEATH.
FT DISULFID 58 71 BY SIMILARITY.
FT DISULFID 61 80 BY SIMILARITY.
FT DISULFID 83 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 141 BY SIMILARITY.
FT DISULFID 144 155 BY SIMILARITY.
FT DISULFID 147 163 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 332 AA; 37592 MW; 5BB03682756BF1B CRC64;

Query Match 60.5%; Score 337; DB 1; Length 332;
Best Local Similarity 63.1%; Pred. No. 1.7e-22;
Matches 65; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 7 LSDVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVLNRWHQ 66
Db 221 IKDVLGKYYITRIAEQMKITEVKGDFVRKNGIGETKIDEIMHNDPKDTAEQKVLNRWYL 280

QY 67 LHGKEAYDVLTIKDLKKNICTLAETKIQTIIILDKITSDSEN 109
Db 281 YHGKDAYCTLIQGLRKAKLSALADKINDIVQKDVTSQENAN 323

RESULT 3
TNR6_BOVIN STANDARD; PRT; 323 AA.
ID TNR6_BOVIN STANDARD; PRT; 323 AA.
AC P51867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96226401; PubMed=8634451;
RA Yoo J., Stone R.T., Beattie C.W.;
RT "Cloning and characterization of the bovine Fas.";
RL DNA Cell Biol. 15:227-234 (1996).
CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -----
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DR EMBL; U34794; AAC48546.1; -.
DR HSP; P25445; 1DDP.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000863; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 323
FT DOMAIN 17 170
FT TRANSMEM 171 188
FT DOMAIN 189 323
FT REPEAT 45 80
FT REPEAT 81 124
FT REPEAT 125 163
FT REPEAT 238 306
FT DOMAIN 238 306
FT DISULFID 45 56
FT DISULFID 57 70
FT DISULFID 60 79
FT DISULFID 82 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 140
FT DISULFID 143 154
FT DISULFID 146 162
FT CARBOHYD 38 38
FT CARBOHYD 115 115
SQ SEQUENCE 323 AA; 36445 MW; 4D88A90E9E1F4892 CRC64;
Query Match 59.4%; Score 331; DB 1; Length 323;
Best Local Similarity 62.6%; Pred. No. 5.7e-22;
Matches 67; Conservative 17; Mismatches 19; Indels 4; Gaps 1;

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QY 5 INLSDVLSKYTTTIGVMTLSQVKGFRKNGVNEAKIDEIKNDVQPTAEQKQLLRNW 64
Db 214 LNLTDVLDLGYPSIAEQMRITEVKEFVRKNGMEAKIDIDIMHNVHETAQKQLLRNW 273
QY 65 HOLGCKEAYDTLIXLKKANLCTAEKIQTLIXDITSDSENSFR 111
Db 274 YOSHGRKNAYTLTKSLPKA----LAEKCIDVMKIDITNERENANLQ 316

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RESULT 4
ID TNR6_MOUSE STANDARD; PRT; 327 AA.
AC P25446; Q9PCQ1;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen
DE (CD95)).
GN TNFRSF6 OR APT1 OR FAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=92148151; PubMed=1371136;
RA Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,
RA Copeland N.G., Jenkins N.A., Nagata S.;
RT "The cDNA structure, expression, and chromosomal assignment of the
RT mouse Fas antigen.";
RL J. Immunol. 148:1274-1279(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Koczan D., Ibrahim S.M., Thiesen H.J.;
RT "Role of a mutant fas receptor in a transgenic mouse.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=93189576; PubMed=7680478;
RA Adachi M., Watanabe-Fukunaga R., Nagata S.;
RT "Aberrant transcription caused by the insertion of an early
RT transposable element in an intron of the Fas antigen gene of lpr
RT mice.";
RN [5]
RP Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
RN [6]
RP INTERACTION WITH DAXX.
RX MEDLINE=97358533; PubMed=9215629;
RA Yang X., Khosravi-Far R., Chang H.Y., Baltimore D.;
RT "Daxx, a novel Fas-binding protein that activates JNK and apoptosis.";
RL Cell 89:1067-1076(1997).
RN [6]
RP VARIANT LPR.
RX MEDLINE=92195401; PubMed=1372394;
RA Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Nagata S.;
RT "Lymphoproliferation disorder in mice explained by defects in Fas
RT antigen that mediates apoptosis.";
RL Nature 356:314-317(1992).
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
CC LIVER, LUNG, HEART, AND ADULT OVARY.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

```

CC CC -!- DISEASE: Defects in TNFRSF6 are the cause of the

CC CC lymphoproliferation phenotype (lpr). lpr mice show lymphadenopathy

CC CC and autoantibody production.

CC CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.

CC CC -!- SIMILARITY: Contains 1 death domain.

CC CC -----

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CC CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC CC -----

CC CC EMBL; M83649; AAA37593.1; -.

CC CC EMBL; AK002590; BAB2211.1; -.

CC CC EMBL; AJ295702; CAC00638.1; -.

CC CC EMBL; AJ295703; CAC00638.1; JOINED.

CC CC EMBL; AJ295704; CAC00638.1; JOINED.

CC CC EMBL; S56490; AAB25700.1; -.

CC CC EMBL; S56485; AAB25700.1; JOINED.

CC CC EMBL; S56486; AAB25700.1; JOINED.

CC CC PIR; A46484; A46484.

CC CC HSP; P25445; 1DDF.

CC CC MGD; MG1:95484; Tnfrsf6.

CC CC InterPro; IPR000488; Death.

CC CC InterPro; IPR008063; Fas\_receptor.

CC CC InterPro; IPR001368; TNFR\_c6.

CC CC Pfam; PF00531; death; 1.

CC CC Pfam; PF00020; TNFR\_c6; 3.

CC CC PRINTS; PR01680; FASRECEPTOR.

CC CC SMART; SM00005; DEATH; 1.

CC CC SMART; SM00208; TNFR; 3.

CC CC PROSITE; PS00652; TNFR\_NGFR\_1; 2.

CC CC PROSITE; PS50050; TNFR\_NGFR\_2; 2.

CC CC PROSITE; PS50017; DEATH\_DOMAIN; 1.

CC CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;

CC CC Disease mutation.

CC CC SIGNAL 1 21

CC CC CHAIN 22 327

CC CC TUMOR NECROSIS FACTOR RECEPTOR

CC CC SUPERFAMILY MEMBER 6.

CC CC EXTRACELLULAR (POTENTIAL).

CC CC TRANSMEM 170 186

CC CC DOMAIN 187 327

CC CC CYTOPLASMIC (POTENTIAL).

CC CC REPEAT 40 79

CC CC TNFR-CYS 1.

CC CC REPEAT 124 162

CC CC TNFR-CYS 3.

CC CC DEATH.

CC CC DISULFID 44 55

CC CC BY SIMILARITY.

CC CC DISULFID 56 69

CC CC BY SIMILARITY.

CC CC DISULFID 59 78

CC CC BY SIMILARITY.

CC CC DISULFID 81 97

CC CC BY SIMILARITY.

CC CC DISULFID 100 115

CC CC BY SIMILARITY.

CC CC DISULFID 103 123

CC CC BY SIMILARITY.

CC CC DISULFID 125 139

CC CC BY SIMILARITY.

CC CC DISULFID 142 153

CC CC BY SIMILARITY.

CC CC DISULFID 145 161

CC CC BY SIMILARITY.

CC CC CARBOHYD 43 43

CC CC N-LINKED (GLCNAC. .) (POTENTIAL).

CC CC CARBOHYD 114 114

CC CC N-LINKED (GLCNAC. .) (POTENTIAL).

CC CC VARIANT 246 246

CC CC I -> N (IN LPR).

CC CC H -> R (IN REF. 3).

CC CC CONFLICT 38 38

CC CC SEQUENCE 327 AA; 37418 MW; F6BFCSACE356EE CRC64;

Query Match 50.0%; Score 278.5; DB 1; Length 327;

Best Local Similarity 50.9%; Pred. No. 2.2e-17;

Matches 57; Conservative 18; Mismatches 34; Indels 3; Gaps 1;

QY 1 ETVAINLSVDLSKYITIAVGMTLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQKVL 60

Db 210 ETIPMNASLSKYPRIAEDMTIQEAKFARENKKEGKIDIMHDSIQDTAEQKVL 269

QY 61 LRWHQLHGKKEAYDTILKDKLANLCTLAETIKDI---TSDSEN 109

Db 270 LLCWYQSHGKSDAYQDLIKGLKKAECRRITLDKFQDMVQKDLGKSTPDTGNEN 321

RESULT 5

TNR6\_RAT

ID TNR6\_RAT STANDARD; PRT; 324 AA.

AC Q63199;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL

DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen

DE (CD95)).

GN TNFRSF6 OR PT1 OR FAS.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Liver;

RC MEDLINE=941128114; PubMed=7507668;

RA Kimura K., Yamamoto M., Wakatsuki T.;

RT "A variant mRNA species encoding a truncated form of Fas antigen in

RT the rat liver.";

RL Biochem. Biophys. Res. Commun. 198:666-674(1994).

CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD

CC recruits caspase-8 to the activated receptor. The resulting death-

CC inducing signaling complex (DISC) performs caspase-8 proteolytic

CC activation which initiates the subsequent cascade of caspases

CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-

CC mediated apoptosis may have a role in the induction of peripheral

CC tolerance, in the antigen-stimulated suicide of mature T-cells, or

CC both (By similarity).

CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,

CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.

CC -!- SIMILARITY: Contains 1 death domain.

CC -----

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL; D26112; BAA05108.1; -.

CC PIR; JC2395; JC2395.

CC HSP; P25445; 1DDF.

CC InterPro; IPR000488; Death.

CC InterPro; IPR008063; Fas\_receptor.

CC InterPro; IPR001368; TNFR\_c6.

CC Pfam; PF00531; death; 1.

CC Pfam; PF00020; TNFR\_c6; 3.

CC PRINTS; PR01680; FASRECEPTOR.

CC SMART; SM00005; DEATH; 1.

CC SMART; SM00208; TNFR; 3.

CC PROSITE; PS00652; TNFR\_NGFR\_1; 2.

CC PROSITE; PS50050; TNFR\_NGFR\_2; 2.

CC PROSITE; PS50017; DEATH\_DOMAIN; 1.

CC Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.

CC SIGNAL 1 21

CC CHAIN 22 324

CC BY SIMILARITY.

CC TUMOR NECROSIS FACTOR RECEPTOR

CC SUPERFAMILY MEMBER 6.

CC EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 22 171

CC DOMAIN 172 188

CC POTENTIAL.

CC DOMAIN 189 324

CC CYTOPLASMIC (POTENTIAL).

CC REPEAT 43 79

CC TNFR-CYS 1.

CC REPEAT 80 123

CC TNFR-CYS 2.

CC REPEAT 124 163

CC TNFR-CYS 3.



Db 628 ATTONLISALNKGSLDLAE-----SLTNDTETNS 657

RESULT 7

RIK1\_MOUSE STANDARD; PRT: 656 AA.

AC Q60855; 08CD90;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)

DE (Serine/threonine protein kinase RIP) (Cell death protein RIP)

DE (Receptor interacting protein).

GN RIPK1 OR RIP OR RINP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

PN [1]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;

RX MEDLINE=22354683; PubMed=12466851;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito K., Suzuki H., Yamana I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher V., Forrest A., Frazer K.S.,

RA Gaesteland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan M.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume M., Inctani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M.,

RA Birney E., Hayashizaki Y.

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs."

RL Nature 420:563-573 (2002).

PN [3]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain, and Liver;

RX MEDLINE=22388257; PubMed=12477932;

RA Klausner R.L., Feingold E.A., Grouse L.H., Shennen C.W., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shennen C.W., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,

RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madao A., Rodriques S., Sanchez A.,

RA Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- FUNCTION: Promotes apoptosis and activation of NF-kappa-B.

CC Required for TNFRSF1A mediated activation of NF-kappa-B.

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -1- SUBUNIT: Binds to the death domain of TNFRSF6 and TRADD. Is

CC recruited by TRADD to TNFRSF1A in a TNF-dependent process. Binds

CC RIPK3, UBE2I1, EGFR, IKBKG, TRAF1, TRAF2 and TRAF3. Interacts

CC with ENL1 (by similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- TISSUE SPECIFICITY: Found at low levels in all tissues.

CC -1- INDUCTION: In Concanavalin A-treated splenocytes.

CC -1- PTM: Proteolytically cleaved by caspase-8 during TNF-induced

CC apoptosis. Cleavage abolishes NF-kappa-B activation and enhances

CC pro-apoptotic signaling through the TRADD-FADD interaction (By

CC similarity).

CC -1- PTM: Autophosphorylated on serine and threonine residues (By

CC similarity).

CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.

CC -1- SIMILARITY: Contains 1 death domain.

CC -----

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CC -----

CC EMBL; U25995; AAB60487.1; -

CC EMBL; AK030959; BAC27194.1; -

CC EMBL; BC050905; AAH50905.1; ALT\_INIT.

CC EMBL; BC054542; AAH54542.1; -

CC EMBL; BC058162; AAH58162.1; -

CC F1R; 149299; 149299.

CC HSP; P25445; 1DDF.

CC MGI; 108212; Ripk1.

CC InterPro; IPR000488; Death.

CC InterPro; IPR000719; Prot\_kinase.

CC InterPro; IPR008271; Ser\_Thr\_pkin\_AS.

CC Pfam; PF00531; death; 1.

CC Pfam; PF00069; pkinase; 1.

CC PRINTS; PR00109; TYRKINASE.

CC ProDom; PD000001; Prot\_kinase; 1.

CC SMART; SM00005; DEATH; 1.

CC PROSITE; PS00108; PROTEIN KINASE ST; 1.

CC PROSITE; PS00117; DEATH DOMAIN; 1.

CC TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;

CC Apoptosis.

FT DOMAIN 17 290 PROTEIN KINASE.

FT NP\_BIND 23 31 ATP (BY SIMILARITY).

FT BINDING 46 46 ATP (BY SIMILARITY).

FT ACT\_SITE 138 138 BY SIMILARITY.

FT DOMAIN 568 654 DEATH.

FT VARIANT 473 473 T -> I.

FT CONFLICT 66 66 M -> K (IN REF. 2).

SQ SEQUENCE 656 AA; 74854 MW; ABB350B523879933 CRC64;

Query Match 14.5%; Score 80.5; DB 1; Length 656;

Best Local Similarity 41.7%; Pred. No. 9.7;

Matches 20; Conservative 3; Mismatches 19; Indels 1; Gaps 1;

QY 27 QVKGFRKNGVNEAKIDEIKNDNVQDTAQKV-QLLRNWHQLHGKKEA 73



Db 582 QWNCARKLGFSTQIDEIDHDYERDLKELKYYQMLQKWLMEGTGA 629

## RESULT 8

TH01 RAT  
ID TH01 RAT STANDARD; PRT; 343 AA.  
AC P59324;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE TH0 complex subunit 1 (tho1) (Nuclear matrix protein p84) (Liver  
regeneration-related protein LRRG175) (Da2-19).  
GN THO1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Liver;  
RA Xu C.S., Li W.Q., Li Y.C., Yan H.M., Chang C.F., Zhao L.F., Ma H.,  
RA Wang L., Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,  
RA Yang K.J., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;  
RT "Liver regeneration after PH.";  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: The THO/TREX complex is recruited to transcribed genes  
CC and travels with the RNA polymerase during elongation. It may  
CC physically link proteins that function in transcription and in RNA  
CC export (By similarity).  
CC -!- SUBUNIT: Part of the heteromultimeric THO/TREX complex containing  
CC THO1, THO2, THO3, THO4 and NXF1/UAP56. Binds to the  
CC hypophosphorylated form of RB1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear in multiple discrete foci and  
CC associated with the nuclear matrix (By similarity).  
CC -!- SIMILARITY: Contains 1 death domain.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; AY325254; AAP92655.1; -;  
DR PROSITE; P550017; DEATH\_DOMAIN; 1.  
KW Transport; mRNA transport; mRNA processing; mRNA splicing;  
KW Nuclear protein; Matrix protein; DNA-binding; RNA-binding.  
FT DOMAIN 248 331 DEATH.  
SQ SEQUENCE 343 AA; 40243 MW; 7AA1C87DE90227BD CRC64;

Query Match 14.1%; Score 78.5; DB 1; Length 343;  
Best Local Similarity 29.7%; Pred. No. 7.3;  
Matches 22; Conservative 13; Mismatches 24; Indels 15; Gaps 2;

QY 44 EIKNDNV-----QQTARQVKQLRNHQLHGKKEAVDTLLKLNKMLCTLAEKIQT 96

Db 271 EIKSDIRQIECYSEDMMKRAQLLVANKQDQGVHETDNLIGALNKSLDLAE----- 325

QY 97 ILKDTSDSENFN 110

Db 326 ---SLTNDTETNSY 336

## RESULT 9

R1K1 HUMAN  
ID R1K1 HUMAN STANDARD; PRT; 671 AA.

AC Q13546; Q13180;

DT 01-NOV-1997 (Rel. 35, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)

DE (Serine/threonine protein kinase RIP) (Cell death protein RIP)  
DE Receptor interacting protein).  
GN RIPK1 OR RIP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AUTOPHOSPHORYLATION, MUTAGENESIS OF LYS-45, AND  
RP INTERACTION WITH TRADD; TRAF1; TRAF2 AND TRAF3.  
RC TISSUE=Umbilical vein endothelial cells;  
RX MEDLINE=96200892; PubMed=8612133;  
RA Hsu H., Huang J., Shu H.-B., Baichwal V.R., Goeddel D.V.;  
RT "TNF-dependent recruitment of the protein kinase RIP to the TNF  
RT receptor-1 signaling complex.";  
RL Immunity 4:387-396(1996).  
RN [2]  
RP REVISION TO 120.  
RA Huang J., Hsu H., Baichwal V.R., Goeddel D.V.;  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Sycamore N.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 300-671 FROM N.A.  
RC TISSUE=Leukemic T-cell;  
RX MEDLINE=95277838; PubMed=7538908;  
RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;  
RT "RIP: a novel protein containing a death domain that interacts with  
RT Fas/APO-1 (CD95) in yeast and causes cell death.";  
RL Cell 81:513-523(1995).  
RN [5]  
RP CLEARANCE BY CASPASE-8, AND MUTAGENESIS OF ASP-324.  
RX MEDLINE=99452794; PubMed=10521396;  
RA Lin Y., Devin A., Rodriguez Y., Liu Z.-G.;  
RT "Cleavage of the death domain kinase RIP by caspase-8 prompts  
RT TNF-induced apoptosis.";  
RL Genes Dev. 13:2514-2526(1999).  
RN [6]  
RP INTERACTION WITH RIPK3.  
RX MEDLINE=98287880; PubMed=10358032;  
RA Sun X., Lee J., Navas T., Baldwin D.T., Stewart T.A., Dixit V.M.;  
RT "RIP3, a novel apoptosis-inducing kinase.";  
RL J. Biol. Chem. 274:16871-16875(1999).  
RN [7]  
RP INTERACTION WITH BNLF1.  
RX MEDLINE=99340272; PubMed=10409763;  
RA Izumi K.M., Cahir McFarland E., Ting A.T., Riley E.A., Seed B.,  
RA Kieff E.D.;  
RT "The Epstein-Barr virus oncoprotein latent membrane protein 1 engages  
RT the tumor necrosis factor receptor-associated proteins TRADD and  
RT receptor-interacting protein (RIP) but does not induce apoptosis or  
RT require RIP for NF-kappaB activation.";  
RL Mol. Cell. Biol. 19:5759-5767(1999).  
RN [8]  
RP INTERACTION WITH IKKKG.  
RX MEDLINE=99128359; PubMed=9927690;  
RA Li Y., Kang J., Friedman J., Tarassishin L., Ye J., Kovalenko A.,  
RA Wallach D., Horwitz M.S.;  
RT "Identification of a cell protein (FIP-3) as a modulator of NF-kappaB  
RT activity and as a target of an adenovirus inhibitor of tumor necrosis  
RT factor alpha-induced apoptosis.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:1042-1047(1999).  
RN [9]  
RP INTERACTION WITH EGFR.  
RX MEDLINE=21153697; PubMed=11116146;  
RA Habib A.A., Chatterjee S., Park S.-K., Ratan R.R., Lefebvre S.,  
RA Vartanian T.;  
RT "The epidermal growth factor receptor engages receptor interacting  
RT protein and nuclear factor-kappa B (NF-kappa B)-inducing kinase to  
RT activate NF-kappa B. Identification of a novel receptor-tyrosine  
RT kinase signalosome.";

J. Biol. Chem. 276:8865-8874 (2001).

[10]

INTERACTION WITH UBCE7IP1.

Chen D., Li X., Zhai Z., Shu H.-B.;

"A novel zinc finger protein interacts with receptor-interacting protein (RIP) and inhibits tumor necrosis factor (TNF)- and I $\kappa$ B-induced NF- $\kappa$ B activation."

J. Biol. Chem. 277:15985-15991 (2002).

-!- FUNCTION: Promotes apoptosis and activation of NF- $\kappa$ B.

-!- Required for TNFRSF1A mediated activation of NF- $\kappa$ B.

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-!- SUBUNIT: Binds to the death domain of TNFRSF6 and TRADD. Is recruited by TRADD to the death domain of a TNF-dependent process. Binds RIPK3, UBCE7IP1, EGFR, I $\kappa$ BK, TRAF1, TRAF2 and TRAF3. Interacts with BNIP1.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- PMM: Proteolytically cleaved by caspase-8 during TNF-induced apoptosis. Cleavage abolishes NF- $\kappa$ B activation and enhances pro-apoptotic signaling through the TRADD-FADD interaction.

-!- PTM: Autophosphorylated on serine and threonine residues.

-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.

-!- SIMILARITY: Contains 1 death domain.

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EMBL; U50062; AAC2232.1; -

EMBL; AL031963; CAD70625.1; -

EMBL; U25994; AAC50137.1; -

PIR; T09479; T09479.

HSP; P08631; IAD5.

Genew; HGNC:10019; RIPK1.

MIM; 603453; -

GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.

GO; GO:0006915; P:apoptosis; TAS.

GO; GO:0007165; P:signal transduction; TAS.

InterPro; IPR000488; Death.

InterPro; IPR000719; Prot\_kinase.

InterPro; IPR008271; Ser\_Thr\_pkin\_AS.

InterPro; IPR001245; Tyr\_kinase.

Pfam; PF00531; death; 1.

Pfam; PF00069; pkinase; 1.

PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Prot\_kinase; 1.

SMART; SM00005; DEATH; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00111; PROTEIN KINASE DOM; 1.

PROSITE; PS00117; DEATH DOMAIN; 1.

Transferrase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; Apoptosis.

DOMAIN 17 289 PROTEIN KINASE.

FT NP\_BIND 23 31 ATP (BY SIMILARITY).

FT BINDING 49 49 ATP (BY SIMILARITY).

FT ACT\_SITE 138 138 BY SIMILARITY.

FT DOMAIN 583 669 DEATH.

FT DOMAIN 411 414 POLY-ARG.

FT SITE 324 325 CLEAVAGE (BY CASPASE-8).

FT MUTAGEN 45 45 K->A: ABOLISHES KINASE ACTIVITY.

FT MUTAGEN 324 324 D->K: ABOLISHES CLEAVAGE BY CASPASE-8.

FT CONFLICT 438 438 V -> A (IN REF. 3).

FT CONFLICT 514 514 V -> S (IN REF. 4).

SEQUENCE 671 AA; 75958 MW; BADC4E7E70456ABE CRC64;

Query Match 14.1%; Score 78.5; DB 1; Length 671;

Best Local Similarity 31.4%; Pred. No. 15;

Matches 22; Conservative 17; Mismatches 28; Indels 3; Gaps 2;

QY 29 KGFRKNGVNEAKIDEIKNDNVQDTARQKV-QLIRNWHQLHGKKEAYDTLIKDKLKNALIC 87

DB 599 KNCARKLGFTSQSIDEDHDYERDLKKEKYQMLQKVMREGIKGA--TVGKLAQALHQ 656

QY 88 TLAEKIQTII 97

DB 657 SRIDLLSSLI 666

RESULT 10

DYHC SCHPO STANDARD; PRT; 4196 AA.

ID DYHC SCHPO

AC OC3230; Q9P6L0; Q9UTP8;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Dynein heavy chain, cytosolic (DYHC).

GN DHC1 OR SPAC1093.06C OR SPAC30C2.01C.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI\_TaxID=4896;

[1]

SEQUENCE FROM N.A.

RP STRAIN=CRL152;

RA Yamamoto A., West R.R., McIntosh J.R., Hiraoka Y.;

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

[2]

SEQUENCE FROM N.A.

RP STRAIN=972;

RC MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Cabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Furnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RA "The genome sequence of Schizosaccharomyces pombe";

Nature 415:871-880 (2002).

RT Nature 415:871-880 (2002).

CC -!- FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular retrograde motility of vesicles and organelles along microtubules. Dynein has ATPase activity; the force-producing power stroke is thought to occur on release of ADP. Required for nuclear movement during meiotic prophase.

CC -!- SUBUNIT: Consists of at least two heavy chains and a number of intermediate and light chains.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Probably binds indirectly to the inner plasma membrane.

CC -!- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem (which binds cargo and interacts with other dynein components), and the head or motor domain. The motor contains six tandemly-linked AAA domains in the head, which form a ring. A stalk-like structure (formed by two of the coiled coil domains) protrudes between AAA 4 and AAA 5 and terminates in a microtubule-binding





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Qy 29 KGFVRK--NGVNEAKIDEIKNDNVQPTAEQKQVLLRNWHQLHGKKEAYDTLKLKXAN 85
Db 103 RGMRSKIMTWVNTKLLDELKKNSHDSDAFISLLI-----YLISKIENNEKIEIYISS 158
Qy 86 LCTLAEKIQIILLIKDITS-----DSNSNF 110
Db 159 VSPFSKVRNVIEKDLRSKRWLTGLIADAFNVSEITTKRLESENTNF 205

RESULT 14
ID_RNS_ECOLI STANDARD; PRT; 265 AA.
AC P16114;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 01-FEB-1994 (Rel. 28, Last annotation update)
DE Regulatory protein rns.
GN RNS.
OS Escherichia coli.
OG Plasmid pDEP23.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128898; PubMed=2563591;
RA Caron J., Coffield L.M., Scott J.R.;
RT "A plasmid-encoded regulatory gene, rns, required for expression of
RT the CS1 and CS2 adhesins of enterotoxigenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:963-967(1989).
CC -!- FUNCTION: REQUIRED FOR THE EXPRESSION OF THE CS1 AND CS2 ADHESINS
CC OF ENTEROTOXIGENIC ESCHERICHIA COLI.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE ARAC/XVLS FAMILY OF TRANSCRIPTIONAL
CC REGULATORS. 94% IDENTICAL TO E. COLI CPAD PROTEIN.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; J04166; AAA24419.1; -.
CC PIR; A31457; A31457.
CC DR InterPro; IPR000005; HTHARAC.
CC DR Pfam; PF00165; HTH_Arac; 2.
CC DR PRINTS; PR00032; HTHARAC.
CC DR SMART; SM00342; HTH_ARAC; 1.
CC DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
CC DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
CC KW Transcription regulation; Activator; DNA-binding; plasmid.
CC FT DNA BIND 180 199 H-T-H MOTIF (BY SIMILARITY).
CC SEQUENCE 265 AA; 30830 MW; 0CFB8A818F60CE CRC64;

Query Match 13.5%; Score 75; DB 1; Length 265;
Best Local Similarity 20.0%; Pred. No. 11;
Matches 26; Conservative 27; Mismatches 41; Indels 36; Gaps 3;

Qy 3 VAINSDVLSKVITTIAGWNTLSQVKGVRKNGVNEAKIDEIKNDNVQPTAEQKQVLLR 62
Db 90 ILYGMSKIDNTACRMSRKIMTTE-----VNKTLDELKKNINSHDNGAFISLLI- 138
Qy 63 NWHQLHGKKEAYDTLKLKXANLCTLAEKIOTIILKDTIS----- 103
Db 139 ---YLISKIENNEKIEIYISSVFFSKVRNLKELKLSRKWLTGITADAFNASEITIR 195
Qy 104 ---DSNSNF 110
Db 196 KRLESENTNF 205
```

```
RESULT 15
CHEA_THEMA STANDARD; PRT; 671 AA.
AC Q56310;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Chemotaxis protein cheA (EC 2.7.3.-).
GN CHEA OR TM0702.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96134983; PubMed=8550470;
RA Swanson R.V., Sanna M.G., Simon M.I.;
RT "Thermotable chemotaxis proteins from the hyperthermophilic
RT bacterium Thermotoga maritima.";
RL J. Bacteriol. 178:484-489(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 293-671.
RX MEDLINE=99142610; PubMed=9989504;
RA Bilwes A.M., Alex L.A., Crane B.R., Simon M.I.;
RT "Structure of CheA, a signal-transducing histidine kinase.";
RL Cell 96:131-141(1999).
CC -!- FUNCTION: INVOLVED IN THE TRANSMISSION OF SENSORY SIGNALS FROM
CC THE CHEMORECEPTORS TO THE FLAGELLAR MOTORS. CHEA IS
CC AUTOPHOSPHORYLATED; IT CAN TRANSFER ITS PHOSPHATE GROUP TO EITHER
CC CHEB OR CHEY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Contains 1 cheW-like domain.
CC -!- SIMILARITY: Contains 1 histidine kinase domain.
CC -!- SIMILARITY: Contains 1 HPT domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U30501; AAA96387.1; -.
CC DR EMBL; AE001741; AAD35784.1; -.
CC PIR; D72346; D72346.
CC DR PDB; 1B3Q; 15-DEC-99.
CC DR PDB; 1I58; 26-AUG-01.
CC DR PDB; 1I59; 26-AUG-01.
CC DR PDB; 1I5A; 26-AUG-01.
CC DR PDB; 1I5B; 26-AUG-01.
CC DR PDB; 1I5C; 26-AUG-01.
CC DR PDB; 1I5D; 26-AUG-01.
CC TIGR; TM0702; -.
CC DR InterPro; IPR003594; ATPbind_ATPase.
CC DR InterPro; IPR004358; Bact_sens_pr_C.
CC DR InterPro; IPR002545; Chew_kinase.
CC DR InterPro; IPR004105; H_kinase_dim.
CC DR InterPro; IPR005467; His_kinase.
CC DR InterPro; IPR008207; Hpt.
CC DR InterPro; IPR008208; Hpt_N.
```

DR Pfam; PF01584; Chew; 1.  
DR Pfam; PF02895; H-kinase\_din; 1.  
DR Pfam; PF02518; HATPase\_C; 1.  
DR Pfam; PF01627; Hpt; 1.  
DR PRINTS; PR00344; BCTFLSENSOR.  
DR ProDom; PD003142; Hpt\_N; 1.  
DR SMART; SM00260; Chew; 1.  
DR SMART; SM00387; HATPase\_C; 1.  
DR SMART; SM00073; HPT; 1.  
DR PROSITE; PS50851; CHEW; 1.  
DR PROSITE; PS50109; HIS\_KIN; 1.  
DR PROSITE; PS50894; HPT; 1.  
KW Sensory transduction; Transferase; Kinase; Phosphorylation;  
KW Chemotaxis; 3d-structure; Complete proteome.  
FT DOMAIN 1 102  
FT DOMAIN 291 541  
FT DOMAIN 543 671  
FT MOD\_RES 45 45  
FT CONFLICT 304 304  
FT STRAND 295 299  
FT HELIX 300 322  
FT TURN 323 324  
FT HELIX 330 354  
FT STRAND 355 357  
FT TURN 358 358  
FT HELIX 359 362  
FT TURN 363 364  
FT HELIX 365 375  
FT TURN 376 377  
FT STRAND 380 385  
FT TURN 387 388  
FT STRAND 390 392  
FT HELIX 393 413  
FT TURN 414 414  
FT HELIX 418 423  
FT TURN 424 425  
FT STRAND 430 439  
FT TURN 440 441  
FT STRAND 442 449  
FT HELIX 456 465  
FT TURN 472 476  
FT TURN 479 479  
FT HELIX 480 483  
FT HELIX 485 487  
FT TURN 489 490  
FT HELIX 508 516  
FT TURN 517 518  
FT STRAND 520 526  
FT TURN 527 529  
FT STRAND 530 538  
FT STRAND 542 551  
FT TURN 552 553  
FT STRAND 554 559  
FT HELIX 560 562  
FT STRAND 563 567  
FT STRAND 570 570  
FT TURN 572 573  
FT STRAND 575 577  
FT TURN 578 579  
FT STRAND 580 585  
FT TURN 586 587  
FT STRAND 588 594  
FT HELIX 595 598  
FT TURN 599 600  
FT STRAND 609 609  
FT TURN 611 617  
FT STRAND 618 619  
FT STRAND 620 626  
FT STRAND 628 637  
FT HELIX 641 644  
FT TURN 645 646  
FT STRAND 650 655  
FT STRAND 661 665

FT HELIX 667  
SQ SEQUENCE 671 AA; 75556 MW; F264398B88DA34E1 CRC64;  
Query Match 13.5%; Score 75; DB 1; Length 671;  
Best Local Similarity 25.6%; Pred. No. 30;  
Matches 30; Conservative 24; Mismatches 45; Indels 18; Gaps 5;  
QY 7 LSDVDLSKY---ITTIAGV--MTLSQVKGFRKGVNKAIDEIKNDNVQDTAEOK---- 57  
DB 234 ISPDVLEKLSSEALSSADIIEVVIKEVTAVTEESGAERTKEETKTEKAERKKVIS 293  
QY 58 -----VOLLRNWHQHGKKE-AYDTLLIKDLKANLCTLAEKIOTIILKDIITSDSEN 107  
DB 294 QTVRVVDIEKLDNLDMLMGLVIAISRILETLKKYNIKELDESLSH--LSRIITLDLQN 348  
Search completed: June 1, 2004, 14:44:30  
Job time : 8.97605 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:35:21 ; Search time 33.2335 Seconds  
(without alignments)

1053.831 Million cell updates/sec

Title: US-09-854-906-9

Perfect score: 557

Sequence: 1 ETVAINLSVDLSKYITIA.....KIQTIIKIDITSDSENSFR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTREMBL\_25:\*

2: sp\_archaea:\*

3: sp\_bacteria:\*

4: sp\_fungi:\*

5: sp\_human:\*

6: sp\_invertebrate:\*

7: sp\_mammal:\*

8: sp\_muc:\*

9: sp\_organelle:\*

10: sp\_phase:\*

11: sp\_plant:\*

12: sp\_rodent:\*

13: sp\_virus:\*

14: sp\_vertebrate:\*

15: sp\_unclassified:\*

16: sp\_rvirus:\*

17: sp\_bacteriap:\*

18: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	515	92.5	109	4	Q81UB7
2	510	91.6	109	4	Q81UB6
3	477	85.6	331	6	Q9TSN4
4	472	84.7	331	6	Q9BDN0
5	472	84.7	333	6	Q9BDP2
6	465	83.5	310	6	Q9GK28
7	465	83.5	331	6	Q9GK36
8	458	82.2	334	6	Q9GL40
9	457	82.0	331	6	Q9BDN4
10	432	77.6	319	6	Q9TV79
11	432	77.6	320	6	Q9X529
12	426	76.5	328	6	Q9BDP0
13	368	66.1	314	6	Q861W6
14	328	58.9	327	6	Q97491
15	186	33.4	285	13	Q9DGH7
16	179	32.1	312	13	Q9DGH8

## ALIGNMENTS

### RESULT 1

Q81UB7 PRELIMINARY; PRT; 109 AA.

AC Q81UB7; 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE CD95 antigen (Fragment).

GN CD95.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22404279; PubMed=12516573;

RA Kurth J., Pernik A., Schmitz R., Iking-Konert C., Chlorazzi N.,

RA Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;

RT "Lack of deleterious somatic mutations in the CD95 gene of

RT plasmablasts from systemic lupus erythematosus patients and

RT autoantibody-producing cell lines.;"

RL Eur. J. Immunol. 32:3785-3792(2002).

DR EMBL; AJ509181; CAD48931.1;

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR000488; Death.

DR Pfam; PF00531; death; 1.

DR SMART; SM00005; DEATH; 1.

DR PROSITE; PS0017; DEATH\_DOMAIN; 1.

FT NON\_TER 1

SQ SEQUENCE 109 AA; 12372 MW; 5EAD927A23C0AAB8 CRC64;

Query Match 92.5%; Score 515; DB 4; Length 109;

Best Local Similarity 100.0%; Pred. No. 2.3e-37;

Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VDSLXVITTIAGWMTLSQVKGFRVKNVNEAKIDIKNDNVQDTAEQVQLLRNHLHG 69

DB 1 VDSLXVITTIAGWMTLSQVKGFRVKNVNEAKIDIKNDNVQDTAEQVQLLRNHLHG 60

17 100.5 18.0 481 9 Q859I9  
18 96 17.2 230 5 Q9N9X2  
19 92.5 16.6 230 16 Q81JR7  
20 92.5 16.6 865 2 Q9XDUL  
21 92.5 16.6 1215 16 Q8XJ10  
22 86.5 15.5 1979 5 Q96133  
23 85 15.3 1435 5 Q81LL4  
24 84.5 15.2 230 16 Q814P0  
25 84 15.1 1754 5 Q812Q1  
26 83 14.9 659 13 Q7ZXL7  
27 83 14.9 709 5 Q81J73  
28 82 14.7 345 3 Q9P972  
29 82 14.7 613 5 Q8IDC0  
30 81.5 14.6 185 2 P94932  
31 81.5 14.6 589 16 Q97FG5  
32 81.5 14.6 937 16 Q89VX9  
33 80.5 14.5 279 2 Q7WT74  
34 80.5 14.5 284 17 Q8TFL5  
35 80 14.4 222 5 Q8IDP5  
36 79.5 14.3 1106 5 Q8IBR5  
37 79 14.2 1132 10 Q9SFG5  
38 78.5 14.1 1193 4 Q92580  
39 78 14.0 530 16 Q8EGB5  
40 78 14.0 610 5 Q9N505  
41 77.5 13.9 572 5 Q9U0N9  
42 77.5 13.9 591 5 Q9GU24  
43 77.5 13.9 660 16 Q8RGT2  
44 77.5 13.9 1558 5 Q96275  
45 77.5 13.9 1786 5 Q9U0P0

Q859I9 staphylococ  
Q9N9X2 geodia cydo  
Q81JR7 bacillus an  
Q9XDUL clostridium  
Q8XJ10 clostridium  
Q96133 plasmodium  
Q81LL4 plasmodium  
Q814P0 bacillus ce  
Q812Q1 plasmodium  
Q7ZXL7 xenopus lae  
Q81J73 plasmodium  
Q9P972 coprinus ci  
Q8IDC0 plasmodium  
P94932 mycoplasma  
Q97FG5 clostridium  
Q89VX9 bradyrhizob  
Q7WT74 marine bact  
Q8TFL5 methanosarc  
Q8IDP5 plasmodium  
Q8IBR5 plasmodium  
Q9SFG5 arabidopsis  
Q92580 homo sapien  
Q8EGB5 shewanelia  
Q9N505 caenorhabdi  
Q9U0N9 plasmodium  
Q9GU24 entamoeba h  
Q8RGT2 fuscobacteri  
Q96275 plasmodium  
Q9U0P0 plasmodium

```
QY 70 KKEAYDTLIKOLKCANCTLAETKIQITILKDIITSDSENSNFR 111
Db 61 KKEAYDTLIKOLKCANCTLAETKIQITILKDIITSDSENSNFR 102

RESULT 2
Q8IUB6
ID Q8IUB6 PRELIMINARY; PRT; 109 AA.
AC Q8IUB6;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE CD95 antigen (fragment).
GN CD95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22404279; PubMed=12516573;
RA Kurth J., Perniok A., Schmitz R., Iking-Konert C., Chiorazzi N.,
RA Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
RT plasmablasts from systemic lupus erythematosus patients and
RT autotubule-producing cell lines."
RL Eur. J. Immunol. 32:3785-3792(2002).
DR EMBL; AJ509182; CAD48932.1; -.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR Pfam; PF00531; death; 1.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
FT NON_TER 1
SQ SEQUENCE 109 AA; 12383 MW; D48D9C942D2044B6 CRC64;

Query Match 91.6%; Score 510; DB 4; Length 109;
Best Local Similarity 99.0%; Pred. No. 6.3e-37;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 VDLISKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHG 69
Db 1 VDLISKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHG 60

QY 70 KKEAYDTLIKOLKCANCTLAETKIQITILKDIITSDSENSNFR 111
Db 61 KKEAYDTLIKOLKCANCTLAETKIQITILKDIITSDSENSNFR 102

RESULT 3
Q9TSN4
ID Q9TSN4 PRELIMINARY; PRT; 331 AA.
AC Q9TSN4;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Death receptor Fas (APO-1/CD95).
GN FAS.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20237686; PubMed=10773350;
RA Murayama Y., Terao K., Inoue-Murayama M.;
RT "Molecular cloning and characterization of cynomolgus monkey Fas.";
RL Hum. Immunol. 61:474-485(2000).
DR EMBL; AB031420; BAA83551.1; -.
DR HSSP; P25445; 1DDF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

QY 70 KKEAYDTLIKOLKCANCTLAETKIQITILKDIITSDSENSNFR 111
Db 61 KKEAYDTLIKOLKCANCTLAETKIQITILKDIITSDSENSNFR 102

Query Match 85.6%; Score 477; DB 6; Length 331;
Best Local Similarity 88.0%; Pred. No. 1.6e-33;
Matches 95; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 4 AINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRN 63
Db 217 AINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRN 276

QY 64 WHQLHGKKEAVDTLIKOLKCANCTLAETKIQITILKDIITSDSENSNFR 111
Db 277 WHQLHGKKEAVDTLIKOLKCANCTLAETKIQITILKDIITSDSENSNFR 324

RESULT 4
Q9BDNO
ID Q9BDNO PRELIMINARY; PRT; 331 AA.
AC Q9BDNO;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE FAS antigen CD95.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.B., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344850; AAK37610.1; -.
DR HSSP; P25445; 1DDF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000863; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 331 AA; 37254 MW; A6CFE3DA12C94765 CRC64;

Query Match 84.7%; Score 472; DB 6; Length 331;
Best Local Similarity 87.9%; Pred. No. 4.3e-33;
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
```





```
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_C6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
SQ SEQUENCE 331 AA; 37167 MW; CE58DB046C67834F CRC64;

Query Match      83.58; Score 465; DB 6; Length 331;
Best Local Similarity 86.9%; Pred. No. 1.7e-32;
Matches 93; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 4 AINLSDVDLSKYTTTITAGVMTLSQVKGKGVNKGVEAKIDEIKNDNVQDTAEQKVLRLN 63
DB AINLSDVDLSKYTTTITAGVMTLSQVKGKGVNKGVEAKIDEIKNDNVQDTAEQKVLRLN 276
QY 64 WHQHGKKEAYDTLLKDLKKNLCTLAETKIQTILLKIDTSDSENSNF 110
DB WHQHGKKEAYDTLLKDLKKNLCTLAETKIQTILLKIDTSDSENSNF 323
QY 277 WYQLHGKKDADCTLLKGLKTADLCTLAETKIHAIVLKIDTSDTENSNF 323
DB WYQLHGKKDADCTLLKGLKTADLCTLAETKIHAIVLKIDTSDTENSNF 323

RESULT 8
Q9GL40 PRELIMINARY; PRT; 334 AA.
AC Q9GL40;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fas antigen.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SHUI B., Chi L., Zhang Y.R.;
RA "Cloning and sequencing of Rhesus monkey Fas antigen cDNA.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY007572; AAGL6762.1; -.
DR HSSP; P25445; 1DDF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_C6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
FT VARIANT 44 44 I -> V.
FT VARIANT 47 47 R -> Q.
FT VARIANT 55 55 E -> D.
FT VARIANT 60 60 R -> H.
FT VARIANT 61 61 N -> S.
FT VARIANT 77 77 E -> G.
FT VARIANT 95 95 G -> A.
FT VARIANT 282 282 E -> G.
FT VARIANT 298 298 G -> D.
FT VARIANT 300 300 C -> *.
SQ SEQUENCE 334 AA; 37531 MW; 2DC5B1661C3191C6 CRC64;

Query Match      82.2%; Score 458; DB 6; Length 334;
Best Local Similarity 86.0%; Pred. No. 7.1e-32;
Matches 92; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 4 AINLSDVDLSKYTTTITAGVMTLSQVKGKGVNKGVEAKIDEIKNDNVQDTAEQKVLRLN 63
DB AINLSDVDLSKYTTTITAGVMTLSQVKGKGVNKGVEAKIDEIKNDNVQDTAEQKVLRLN 279
QY 64 WHQHGKKEAYDTLLKDLKKNLCTLAETKIQTILLKIDTSDSENSNF 110
DB WHQHGKKEAYDTLLKDLKKNLCTLAETKIQTILLKIDTSDSENSNF 326
DB WYQHGKKDADCTLLKGLKTADLCTLAETKIHAIVLKIDTSDTENSNF 326

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OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Isono T., Tanbe Y., Nagano Y., Seto A.;  
RT "Splicing and allelic variation in the rabbit Fas antigen gene."  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB021296; BAA78430.1; -  
DR HSP; P25445; 1DDF.

DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.  
DR GO; GO:0006955; P:immune response; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.

DR InterPro; IPR008063; Fas receptor.  
DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 3.

DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS50017; DEATH DOMAIN; 1.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
SQ SEQUENCE 319 AA; 35961 MW; 06FA0033B1846591 CRC64;

Query Match 77.6%; Score 432; DB 6; Length 319;  
Best Local Similarity 75.7%; Pred. No. 1.2e-29;  
Matches 84; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
Db 200 EGVPMNFSDVDISKYIPTTAEMKINEVFEVRKNGVNEAKIDEIKNDNIQDTAEQKVL 259

QY 61 LRNHQHLGKGEAYDTLKLKCANLCTLAETIQTILKIDITSSENSNR 111  
Db 260 LRNHQHLGKGDAYNTLKLKCANLCTLAETIQTILKIDITSSENSNR 310

RESULT 11  
QX529 ID QX529 PRELIMINARY; PRT; 320 AA.

AC QX529;  
DT 01-NOV-1999 (T-EMBLrel. 12, Created)

DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE C-type Fas antigen.  
OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Isono T., Tanbe Y., Nagano Y., Seto A.;

RT "Splicing and allelic variation in the rabbit Fas antigen gene."  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB021296; BAA78431.1; -  
DR EMBL; AB021296; BAA78428.1; -

DR HSP; P25445; 1DDF.  
DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0006915; P:apoptosis; IEA.

DR GO; GO:0006955; P:immune response; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR000488; Death.  
DR InterPro; IPR008063; Fas receptor.

DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; death; 1.

DR Pfam; PF00020; TNFR\_c6; 3.  
DR PRINTS; PR01680; FASRECEPTOR.

DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS50017; DEATH DOMAIN; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
SQ SEQUENCE 320 AA; 36102 MW; DA235E243220FFB3 CRC64;

Query Match 77.6%; Score 432; DB 6; Length 320;  
Best Local Similarity 75.7%; Pred. No. 1.2e-29;  
Matches 84; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
Db 201 EGVPMNFSDVDISKYIPTTAEMKINEVFEVRKNGVNEAKIDEIKNDNIQDTAEQKVL 260

QY 61 LRNHQHLGKGEAYDTLKLKCANLCTLAETIQTILKIDITSSENSNR 111  
Db 261 LRNHQHLGKGDAYNTLKLKCANLCTLAETIQTILKIDITSSENSNR 311

RESULT 12  
Q9BDP0 ID Q9BDP0 PRELIMINARY; PRT; 328 AA.

AC Q9BDP0;  
DT 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE FAS antigen CD95.  
OS Aotus trivirgatus (Night monkey) (Douroucoul).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OX NCBI\_TaxID=9505;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=21383618; PubMed=11491535;  
RA Villinger F., Boslik P., Wayne A.E., King C.L., Genain C.P.,  
RA Weiss W.R., Ansari A.A.;

RT "Cloning, sequencing, and homology analysis of nonhuman primate  
RT Fas/Fas-ligand and co-stimulatory molecules."  
RL Immunogenetics 53:315-328 (2001).

DR EMBL; AF344835; AAK37531.1; -  
DR HSP; P25445; 1DDF.

DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.  
DR GO; GO:0006955; P:immune response; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.

DR InterPro; IPR008063; Fas receptor.  
DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 2.

DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS50017; DEATH DOMAIN; 1.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
FT VARIANT 157 157 S -> T.

SQ SEQUENCE 328 AA; 37332 MW; B3DED1DAC97D6353 CRC64;

Query Match 76.5%; Score 426; DB 6; Length 328;  
Best Local Similarity 78.4%; Pred. No. 4.2e-29;  
Matches 87; Conservative 8; Mismatches 12; Indels 4; Gaps 1;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVL 60  
Db 213 ETVPMLNSVDLSKYITVIAEHMTISQVDFVRKNGVNEAKIDEIKNDNIQDTAEQKVL 272

QY 61 LRNHQHLGKGEAYDTLKLKCANLCTLAETIQTILKIDITSSENSNR 111  
Db 273 LRNHQHLGKGDAYNTLKLKCANLCTLAETIQTILKIDITSSENSNR 319

RESULT 13  
Q861W6 ID Q861W6 PRELIMINARY; PRT; 314 AA.

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AC Q861W6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fas antigen.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99053606; PubMed=9839871;
RA Mizuno T., Endo Y., Momoi Y., Goto Y., Nishimura Y., Taubota K.,
RA Mikami T., Ohno K., Watari T., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning of feline Fas antigen and Fas ligand cDNAs.";
RL Vet. Immunol. Immunopathol. 65:161-172(1998).
DR EMBL: AB009279; BAC76425.1; -
DR GO: GO:0016020; C-membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000488; Death.
DR InterPro: IPR008063; Fas_receptor.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR PRINTS: PR01680; FASRECEPTOR.
DR SMART: SM00208; TNFR; 3.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 314 AA; 35046 MW; 0B35FCFF720D3953 CRC64;

Query Match 66.1%; Score 368; DB 6; Length 314;
Best Local Similarity 67.8%; Pred. No. 4.3e-24;
Matches 69; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTAGVMTLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQKVL 60
Db 212 ESNPMFTDLSKYISSAEQMKITQVFEVRKNGINEAKIDEIKNDNLQDTAEQKVL 271
QY 61 LRNWHQHGKKEAYDTLIKDKKANLCTLAETKIQTIIKIDITS 103
Db 272 LRNWHQHGKKEAYDTLIKDKKANLCTLAETKIQTIIKIDITS 314

RESULT 14
O97491
ID O97491 PRELIMINARY; PRT; 327 AA.
AC O97491;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fas protein.
GN FAS.
OS Evis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lymphocytes;
RA Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RT "Cloning of sheep fas antigen.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB011671; BRA37093.1; -
DR HSSP: P25445; 1DDF.
DR GO: GO:0016020; C-membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0006955; P:immune response; IEA.

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DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000488; Death.
DR InterPro: IPR008063; Fas_receptor.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 3.
DR PRINTS: PR01680; FASRECEPTOR.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 327 AA; 36928 MW; 5CFEE844B2EE387A CRC64;

Query Match 58.9%; Score 328; DB 6; Length 327;
Best Local Similarity 61.7%; Pred. No. 1.3e-20;
Matches 66; Conservative 19; Mismatches 18; Indels 4; Gaps 1;

QY 5 INLSVDLSKYITTTAGVMTLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQKVL 64
Db 218 LNLTDVDLQKYPISIAELMKITEVKEFVRKNGVEAKIDIMHDLHETAEQKVL 277
QY 65 HOLHGKKEAYDTLIKDKKANLCTLAETKIQTIIKIDITS 111
Db 278 YSHGKKNAYCTTNNLPK----LAEKIDIVLKDIINERENANLQ 320

RESULT 15
O9DGH7
ID O9DGH7 PRELIMINARY; PRT; 285 AA.
AC O9DGH7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fas ligand receptor soluble form (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Brigham J.T., Johnson A.L.;
RT "Fas Expression and Regulation in Hen Granulosa Cells.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF296875; AAG02243.1; -
DR HSSP: Q92956; 1JMA.
DR GO: GO:0016020; C-membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000488; Death.
DR InterPro: IPR008063; Fas_receptor.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 2.
DR PRINTS: PR01680; FASRECEPTOR.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 285 AA; 32431 MW; A9761960CCD79E6D CRC64;

Query Match 33.4%; Score 186; DB 13; Length 285;
Best Local Similarity 38.7%; Pred. No. 2.4e-08;
Matches 41; Conservative 22; Mismatches 43; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTAGVMTLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQKVL 60
Db 140 ETLRLIHIDVDLTHVPDIVREMTLEQWTFVRRHRLSEPTTEETLLDNNSTSEQIKL 199
QY 61 LRNWHQHGKKEAYDTLIKDKKANLCTLAETKIQTIIKIDITS 106

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Db 200 FORWYQKHGMGGAYETLICSRLDLKVRTAADKIERKLAACVCSHQE 245

Search completed: June 1, 2004, 14:46:22  
Job time : 34.2335 secs